

SEQUENCE LISTING

<110> Garvan Institute of Medical Research

<120> Novel Translocation Assay

<130> 502551/PXM

<150> AU2003904237

<151> 2003-08-08

<160> 64

<170> PatentIn version 3.1

<210> 1

<211> 2128

<212> DNA

<213> GLUT4

<220>

<221> CDS

<222> (146)..(1672)

<223>

<400> 1

```

gggggtccca tcgggcccgc cctcgcacgt cactccggga cccccgcggc ctccgtaggt      60
tctgcgctcc aggccggagt cagagactcc aggatcggtt ctttcattctt cgccgcccct      120
gcgcgtccag ctcttctaag acgag atg ccg tcg ggc ttc caa cag ata ggc      172
                        Met Pro Ser Gly Phe Gln Gln Ile Gly
                        1                      5

tcc gaa gat ggg gaa ccc cct cag cag cga gtg act ggg acc ctg gtc      220
Ser Glu Asp Gly Glu Pro Pro Gln Gln Arg Val Thr Gly Thr Leu Val
10                      15                      20                      25

ctt gct gtg ttc tct gcg gtg ctt ggc tcc ctg cag ttt ggg tac aac      268
Leu Ala Val Phe Ser Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn
30                      35                      40

att ggg gtc atc aat gcc cct cag aag gtg att gaa cag agc tac aat      316
Ile Gly Val Ile Asn Ala Pro Gln Lys Val Ile Glu Gln Ser Tyr Asn
45                      50                      55

gag acg tgg ctg ggg agg cag ggg cct gag gga ccc agc tcc atc cct      364
Glu Thr Trp Leu Gly Arg Gln Gly Pro Glu Gly Pro Ser Ser Ile Pro
60                      65                      70

cca ggc acc ctc acc acc ctc tgg gcc ctc tcc gtg gcc atc ttt tcc      412
Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser Val Ala Ile Phe Ser
75                      80                      85

gtg ggc ggc atg att tcc tcc ttc ctc att ggt atc atc tct cag tgg      460
Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly Ile Ile Ser Gln Trp
90                      95                      100                      105

ctt gga agg aaa agg gcc atg ctg gtc aac aat gtc ctg gcg gtg ctg      508
Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn Val Leu Ala Val Leu
110                      115                      120

ggg ggc agc ctc atg ggc ctg gcc aac gct gct gcc tcc tat gaa atg      556

```

Gly	Gly	Ser	Leu	Met	Gly	Leu	Ala	Asn	Ala	Ala	Ala	Ser	Tyr	Glu	Met	
			125					130					135			
ctc	atc	ctt	gga	cga	ttc	ctc	att	ggc	gcc	tac	tca	ggg	ctg	aca	tca	604
Leu	Ile	Leu	Gly	Arg	Phe	Leu	Ile	Gly	Ala	Tyr	Ser	Gly	Leu	Thr	Ser	
		140					145					150				
ggg	ctg	gtg	ccc	atg	tac	gtg	ggg	gag	att	gct	ccc	act	cac	ctg	cgg	652
Gly	Leu	Val	Pro	Met	Tyr	Val	Gly	Glu	Ile	Ala	Pro	Thr	His	Leu	Arg	
	155					160					165					
ggc	gcc	ctg	ggg	acg	ctc	aac	caa	ctg	gcc	att	gtt	atc	ggc	att	ctg	700
Gly	Ala	Leu	Gly	Thr	Leu	Asn	Gln	Leu	Ala	Ile	Val	Ile	Gly	Ile	Leu	
170					175					180					185	
atc	gcc	cag	gtg	ctg	ggc	ttg	gag	tcc	ctc	ctg	ggc	act	gcc	agc	ctg	748
Ile	Ala	Gln	Val	Leu	Gly	Leu	Glu	Ser	Leu	Leu	Gly	Thr	Ala	Ser	Leu	
				190					195					200		
tgg	cca	ctg	ctc	ctg	ggc	ctc	aca	gtg	cta	cct	gcc	ctc	ctg	cag	ctg	796
Trp	Pro	Leu	Leu	Leu	Gly	Leu	Thr	Val	Leu	Pro	Ala	Leu	Leu	Gln	Leu	
			205					210					215			
gtc	ctg	ctg	ccc	ttc	tgt	ccc	gag	agc	ccc	cgc	tac	ctc	tac	atc	atc	844
Val	Leu	Leu	Pro	Phe	Cys	Pro	Glu	Ser	Pro	Arg	Tyr	Leu	Tyr	Ile	Ile	
		220					225					230				
cag	aat	ctc	gag	ggg	cct	gcc	aga	aag	agt	ctg	aag	cgc	ctg	aca	ggc	892
Gln	Asn	Leu	Glu	Gly	Pro	Ala	Arg	Lys	Ser	Leu	Lys	Arg	Leu	Thr	Gly	
	235					240					245					
tgg	gcc	gat	gtt	tct	gga	gtg	ctg	gct	gag	ctg	aag	gat	gag	aag	cgg	940
Trp	Ala	Asp	Val	Ser	Gly	Val	Leu	Ala	Glu	Leu	Lys	Asp	Glu	Lys	Arg	
250					255					260					265	
aag	ctg	gag	cgt	gag	cgg	cca	ctg	tcc	ctg	ctc	cag	ctc	ctg	ggc	agc	988
Lys	Leu	Glu	Arg	Glu	Arg	Pro	Leu	Ser	Leu	Leu	Gln	Leu	Leu	Gly	Ser	
				270					275					280		
cgt	acc	cac	cgg	cag	ccc	ctg	atc	att	gcg	gtc	gtg	ctg	cag	ctg	agc	1036
Arg	Thr	His	Arg	Gln	Pro	Leu	Ile	Ile	Ala	Val	Val	Leu	Gln	Leu	Ser	
			285					290					295			
cag	cag	ctc	tct	ggc	atc	aat	gct	gtt	ttc	tat	tat	tcg	acc	agc	atc	1084
Gln	Gln	Leu	Ser	Gly	Ile	Asn	Ala	Val	Phe	Tyr	Tyr	Ser	Thr	Ser	Ile	
		300					305					310				
ttc	gag	aca	gca	ggg	gta	ggc	cag	cct	gcc	tat	gcc	acc	ata	gga	gct	1132
Phe	Glu	Thr	Ala	Gly	Val	Gly	Gln	Pro	Ala	Tyr	Ala	Thr	Ile	Gly	Ala	
	315					320					325					
ggt	gtg	gtc	aac	aca	gtc	ttc	acc	ttg	gtc	tcg	gtg	ttg	ttg	gtg	gag	1180
Gly	Val	Val	Asn	Thr	Val	Phe	Thr	Leu	Val	Ser	Val	Leu	Leu	Val	Glu	
330					335					340					345	
cgg	gcg	ggg	cgc	cgg	acg	ctc	cat	ctc	ctg	ggc	ctg	gcg	ggc	atg	tgt	1228
Arg	Ala	Gly	Arg	Arg	Thr	Leu	His	Leu	Leu	Gly	Leu	Ala	Gly	Met	Cys	
				350					355					360		
ggc	tgt	gcc	atc	ctg	atg	act	gtg	gct	ctg	ctc	ctg	ctg	gag	cga	gtt	1276
Gly	Cys	Ala	Ile	Leu	Met	Thr	Val	Ala	Leu	Leu	Leu	Leu	Glu	Arg	Val	
			365					370					375			

cca gcc atg agc tac gtc tcc att gtg gcc atc ttt ggc ttc gtg gca 1324
 Pro Ala Met Ser Tyr Val Ser Ile Val Ala Ile Phe Gly Phe Val Ala
 380 385 390

ttt ttt gag att ggc cct ggc ccc att cct tgg ttc atc gtg gcc gag 1372
 Phe Phe Glu Ile Gly Pro Gly Pro Ile Pro Trp Phe Ile Val Ala Glu
 395 400 405

ctc ttc agc cag gga ccc cgc ccg gca gcc atg gct gtg gct ggt ttc 1420
 Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Met Ala Val Ala Gly Phe
 410 415 420 425

tcc aac tgg acg agc aac ttc atc att ggc atg ggt ttc cag tat gtt 1468
 Ser Asn Trp Thr Ser Asn Phe Ile Ile Gly Met Gly Phe Gln Tyr Val
 430 435 440

gcg gag gct atg ggg ccc tac gtc ttc ctt cta ttt gcg gtc ctc ctg 1516
 Ala Glu Ala Met Gly Pro Tyr Val Phe Leu Leu Phe Ala Val Leu Leu
 445 450 455

ctg ggc ttc ttc atc ttc acc ttc tta aga gta cct gaa act cga ggc 1564
 Leu Gly Phe Phe Ile Phe Thr Phe Leu Arg Val Pro Glu Thr Arg Gly
 460 465 470

cgg acg ttt gac cag atc tca gct gcc ttc cac cgg aca ccc tct ctt 1612
 Arg Thr Phe Asp Gln Ile Ser Ala Ala Phe His Arg Thr Pro Ser Leu
 475 480 485

tta gag cag gag gtg aaa ccc agc aca gaa ctt gag tat tta ggg cca 1660
 Leu Glu Gln Glu Val Lys Pro Ser Thr Glu Leu Glu Tyr Leu Gly Pro
 490 495 500 505

gat gag aac gac tgaggggcca ggcaggggtg ggagagccag ctctctctac 1712
 Asp Glu Asn Asp

ccggcccaga gacccttccc tttcctctgc agcactttaa ccctctcttc cctattattt 1772

ccgggtggaa aagaatccct gcagcctggt agaattggga agctggggga aggggtgtct 1832

gagcaccccc tcattcccct cgtgtgactc tcttgatta tttatgtgtt gtggtttggc 1892

cgtggccatc aggggtgggc actctcccct ccctcttcct tccccatcc cctttcctcc 1952

ccaccttccc cagactcagc tocagaatac cttcttcgct gctagagaag ggggattgga 2012

gggaagacag gtctagactt tctcagtggy acaaaccaga gcagagagca ggacaggaga 2072

caagaaatcc agtttccac caccttgac tcctcccaca atctgggact ttact 2128

<210> 2
 <211> 509
 <212> PRT
 <213> GLUT4

<400> 2

Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
 1 5 10 15

Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val

Leu Ala Glu Leu Lys Asp Glu Lys Arg Lys Leu Glu Arg Glu Arg Pro
260 265 270

Leu Ser Leu Leu Gln Leu Leu Gly Ser Arg Thr His Arg Gln Pro Leu
 275 280 285

Ile Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn
 290 295 300

Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Thr Ala Gly Val Gly
 305 310 315 320

Gln Pro Ala Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Val Phe
 325 330 335

Thr Leu Val Ser Val Leu Leu Val Glu Arg Ala Gly Arg Arg Thr Leu
 340 345 350

His Leu Leu Gly Leu Ala Gly Met Cys Gly Cys Ala Ile Leu Met Thr
 355 360 365

Val Ala Leu Leu Leu Leu Glu Arg Val Pro Ala Met Ser Tyr Val Ser
 370 375 380

Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly
 385 390 395 400

Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg
 405 410 415

Pro Ala Ala Met Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
 420 425 430

Ile Ile Gly Met Gly Phe Gln Tyr Val Ala Glu Ala Met Gly Pro Tyr
 435 440 445

Val Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr
 450 455 460

Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser
 465 470 475 480

Ala Ala Phe His Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro
 485 490 495

Ser Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu Asn Asp
 500 505

<210> 3
 <211> 1566
 <212> DNA

<213> HA tagged GLUT4

<220>

<221> CDS

<222> (1)..(1566)

<223>

<400> 3

atg ccg tcg ggc ttc caa cag ata ggc tcc gaa gat ggg gaa ccc cct	48
Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro	
1 5 10 15	
cag cag cga gtg act ggg acc ctg gtc ctt gct gtg ttc tct gcg gtg	96
Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val	
20 25 30	
ctt ggc tcc ctg cag ttt ggg tac aac att ggg gtc atc aat gcc cct	144
Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro	
35 40 45	
cag aag gtg att gaa cag agc tac aat gag acg tgg ctg ggg agg cag	192
Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln	
50 55 60	
ggg cct gag atc gat tat cct tat gat gtt cct gat tat gct gag gga	240
Gly Pro Glu Ile Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Glu Gly	
65 70 75 80	
ccc agc tcc atc cct cca ggc acc ctc acc acc ctc tgg gcc ctc tcc	288
Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser	
85 90 95	
gtg gcc atc ttt tcc gtg ggc ggc atg att tcc tcc ttc ctc att ggt	336
Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly	
100 105 110	
atc atc tct cag tgg ctt gga agg aaa agg gcc atg ctg gtc aac aat	384
Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn	
115 120 125	
gtc ctg gcg gtg ctg ggg ggc agc ctc atg ggc ctg gcc aac gct gct	432
Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala	
130 135 140	
gcc tcc tat gaa atg ctc atc ctt gga cga ttc ctc att ggc gcc tac	480
Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr	
145 150 155 160	
tca ggg ctg aca tca ggg ctg gtg ccc atg tac gtg ggg gag att gct	528
Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala	
165 170 175	
ccc act cac ctg cgg ggc gcc ctg ggg acg ctc aac caa ctg gcc att	576
Pro Thr His Leu Arg Gly Ala Leu Gly Thr Leu Asn Gln Leu Ala Ile	
180 185 190	
gtt atc ggc att ctg atc gcc cag gtg ctg ggc ttg gag tcc ctc ctg	624
Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly Leu Glu Ser Leu Leu	
195 200 205	
ggc act gcc agc ctg tgg cca ctg ctc ctg ggc ctc aca gtg cta cct	672
Gly Thr Ala Ser Leu Trp Pro Leu Leu Leu Gly Leu Thr Val Leu Pro	
210 215 220	

gcc ctc ctg cag ctg gtc ctg ctg ccc ttc tgt ccc gag agc ccc cgc Ala Leu Leu Gln Leu Val Leu Leu Pro Phe Cys Pro Glu Ser Pro Arg 225 230 235 240	720
tac ctc tac atc atc cag aat ctc gag ggg cct gcc aga aag agt ctg Tyr Leu Tyr Ile Ile Gln Asn Leu Glu Gly Pro Ala Arg Lys Ser Leu 245 250 255	768
aag cgc ctg aca ggc tgg gcc gat gtt tct gga gtg ctg gct gag ctg Lys Arg Leu Thr Gly Trp Ala Asp Val Ser Gly Val Leu Ala Glu Leu 260 265 270	816
aag gat gag aag cgg aag ctg gag cgt gag cgg cca ctg tcc ctg ctc Lys Asp Glu Lys Arg Lys Leu Glu Arg Glu Arg Pro Leu Ser Leu Leu 275 280 285	864
cag ctc ctg ggc agc cgt acc cac cgg cag ccc ctg atc att gcg gtc Gln Leu Leu Gly Ser Arg Thr His Arg Gln Pro Leu Ile Ile Ala Val 290 295 300	912
gtg ctg cag ctg agc cag cag ctc tct ggc atc aat gct gtt ttc tat Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr 305 310 315 320	960
tat tcg acc agc atc ttc gag aca gca ggg gta ggc cag cct gcc tat Tyr Ser Thr Ser Ile Phe Glu Thr Ala Gly Val Gly Gln Pro Ala Tyr 325 330 335	1008
gcc acc ata gga gct ggt gtg gtc aac aca gtc ttc acc ttg gtc tcg Ala Thr Ile Gly Ala Gly Val Val Asn Thr Val Phe Thr Leu Val Ser 340 345 350	1056
gtg ttg ttg gtg gag cgg gcg ggg cgc cgg acg ctc cat ctc ctg ggc Val Leu Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Leu Leu Gly 355 360 365	1104
ctg gcg ggc atg tgt ggc tgt gcc atc ctg atg act gtg gct ctg ctc Leu Ala Gly Met Cys Gly Cys Ala Ile Leu Met Thr Val Ala Leu Leu 370 375 380	1152
ctg ctg gag cga gtt cca gcc atg agc tac gtc tcc att gtg gcc atc Leu Leu Glu Arg Val Pro Ala Met Ser Tyr Val Ser Ile Val Ala Ile 385 390 395 400	1200
ttt ggc ttc gtg gca ttt ttt gag att ggc cct ggc ccc att cct tgg Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro Ile Pro Trp 405 410 415	1248
ttc atc gtg gcc gag ctc ttc agc cag gga ccc cgc ccg gca gcc atg Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Met 420 425 430	1296
gct gtg gct ggt ttc tcc aac tgg acg agc aac ttc atc att ggc atg Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe Ile Ile Gly Met 435 440 445	1344
ggt ttc cag tat gtt gcg gag gct atg ggg ccc tac gtc ttc ctt cta Gly Phe Gln Tyr Val Ala Glu Ala Met Gly Pro Tyr Val Phe Leu Leu 450 455 460	1392
ttt gcg gtc ctc ctg ctg ggc ttc ttc atc ttc acc ttc tta aga gta Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr Phe Leu Arg Val	1440

8

465 470 475 480
 cct gaa act cga ggc cgg acg ttt gac cag atc tca gct gcc ttc cac 1488
 Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser Ala Ala Phe His
 485 490 495
 cgg aca ccc tct ctt tta gag cag gag gtg aaa ccc agc aca gaa ctt 1536
 Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro Ser Thr Glu Leu
 500 505 510
 gag tat tta ggg cca gat gag aac gac tga 1566
 Glu Tyr Leu Gly Pro Asp Glu Asn Asp
 515 520

 <210> 4
 <211> 521
 <212> PRT
 <213> HA tagged GLUT4

 <400> 4
 Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
 1 5 10 15

 Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
 20 25 30

 Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
 35 40 45

 Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
 50 55 60

 Gly Pro Glu Ile Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Glu Gly
 65 70 75 80

 Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser
 85 90 95

 Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly
 100 105 110

 Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn
 115 120 125

 Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala
 130 135 140

 Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr
 145 150 155 160

 Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala

165	170	175
Pro Thr His Leu Arg Gly Ala Leu Gly Thr Leu Asn Gln Leu Ala Ile 180 185 190		
Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly Leu Glu Ser Leu Leu 195 200 205		
Gly Thr Ala Ser Leu Trp Pro Leu Leu Leu Gly Leu Thr Val Leu Pro 210 215 220		
Ala Leu Leu Gln Leu Val Leu Leu Pro Phe Cys Pro Glu Ser Pro Arg 225 230 235 240		
Tyr Leu Tyr Ile Ile Gln Asn Leu Glu Gly Pro Ala Arg Lys Ser Leu 245 250 255		
Lys Arg Leu Thr Gly Trp Ala Asp Val Ser Gly Val Leu Ala Glu Leu 260 265 270		
Lys Asp Glu Lys Arg Lys Leu Glu Arg Glu Arg Pro Leu Ser Leu Leu 275 280 285		
Gln Leu Leu Gly Ser Arg Thr His Arg Gln Pro Leu Ile Ile Ala Val 290 295 300		
Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr 305 310 315 320		
Tyr Ser Thr Ser Ile Phe Glu Thr Ala Gly Val Gly Gln Pro Ala Tyr 325 330 335		
Ala Thr Ile Gly Ala Gly Val Val Asn Thr Val Phe Thr Leu Val Ser 340 345 350		
Val Leu Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Leu Leu Gly 355 360 365		
Leu Ala Gly Met Cys Gly Cys Ala Ile Leu Met Thr Val Ala Leu Leu 370 375 380		
Leu Leu Glu Arg Val Pro Ala Met Ser Tyr Val Ser Ile Val Ala Ile 385 390 395 400		
Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro Ile Pro Trp 405 410 415		

10

Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Met
 420 425 430

Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe Ile Ile Gly Met
 435 440 445

Gly Phe Gln Tyr Val Ala Glu Ala Met Gly Pro Tyr Val Phe Leu Leu
 450 455 460

Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr Phe Leu Arg Val
 465 470 475 480

Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser Ala Ala Phe His
 485 490 495

Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro Ser Thr Glu Leu
 500 505 510

Glu Tyr Leu Gly Pro Asp Glu Asn Asp
 515 520

<210> 5
 <211> 512
 <212> PRT
 <213> GLUT4 TAIL mutant

<400> 5

Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
 1 5 10 15

Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
 20 25 30

Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
 35 40 45

Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
 50 55 60

Gly Pro Glu Ile Asp Glu Gly Pro Ser Ser Ile Pro Pro Gly Thr Leu
 65 70 75 80

Thr Thr Leu Trp Ala Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met
 85 90 95

Ile Ser Ser Phe Leu Ile Gly Ile Ile Ser Gln Trp Leu Gly Arg Lys
 100 105 110

Arg Ala Met Leu Val Asn Asn Val Leu Ala Val Leu Gly Gly Ser Leu
 115 120 125

Met Gly Leu Ala Asn Ala Ala Ala Ser Tyr Glu Met Leu Ile Leu Gly
 130 135 140

Arg Phe Leu Ile Gly Ala Tyr Ser Gly Leu Thr Ser Gly Leu Val Pro
 145 150 155 160

Met Tyr Val Gly Glu Ile Ala Pro Thr His Leu Arg Gly Ala Leu Gly
 165 170 175

Thr Leu Asn Gln Leu Ala Ile Val Ile Gly Ile Leu Ile Ala Gln Val
 180 185 190

Leu Gly Leu Glu Ser Leu Leu Gly Thr Ala Ser Leu Trp Pro Leu Leu
 195 200 205

Leu Gly Leu Thr Val Leu Pro Ala Leu Leu Gln Leu Val Leu Leu Pro
 210 215 220

Phe Cys Pro Glu Ser Pro Arg Tyr Leu Tyr Ile Ile Gln Asn Leu Glu
 225 230 235 240

Gly Pro Ala Arg Lys Ser Leu Lys Arg Leu Thr Gly Trp Ala Asp Val
 245 250 255

Ser Gly Val Leu Ala Glu Leu Lys Asp Glu Lys Arg Lys Leu Glu Arg
 260 265 270

Glu Arg Pro Leu Ser Leu Leu Gln Leu Leu Gly Ser Arg Thr His Arg
 275 280 285

Gln Pro Leu Ile Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser
 290 295 300

Gly Ile Asn Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Thr Ala
 305 310 315 320

Gly Val Gly Gln Pro Ala Tyr Ala Thr Ile Gly Ala Gly Val Val Asn
 325 330 335

Thr Val Phe Thr Leu Val Ser Val Leu Leu Val Glu Arg Ala Gly Arg
 340 345 350

Arg Thr Leu His Leu Leu Gly Leu Ala Gly Met Cys Gly Cys Ala Ile
 355 360 365

Leu Met Thr Val Ala Leu Leu Leu Glu Arg Val Pro Ala Met Ser
370 375 380

Tyr Val Ser Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile
385 390 395 400

Gly Pro Gly Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln
405 410 415

Gly Pro Arg Pro Ala Ala Met Ala Val Ala Gly Phe Ser Asn Trp Thr
420 425 430

Ser Asn Phe Ile Ile Gly Met Gly Phe Gln Tyr Val Ala Glu Ala Met
435 440 445

Gly Pro Tyr Val Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe
450 455 460

Ile Phe Thr Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp
465 470 475 480

Gln Ile Ser Ala Ala Phe His Arg Thr Pro Ser Leu Leu Glu Gln Glu
485 490 495

Val Lys Pro Ser Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn Val
500 505 510

<210> 6
<211> 512
<212> PRT
<213> HA tagged GLUT4 TAIL mutant
MPSGFQQIGSEDEPPQQRVTGTLVLAVFSAVLGSQFGYNIGVINAPQKVIEQSYNETWLGRQGPEIDYPYDVPDYAE
GPSSIPPGLTTLWALSVAIFSVGGMISSFLIGIISQWLGRKRAMLVNNVLAVLGGSLMGLANAAASYEMLILGRFLIG
AYSGLTSGLVPMYVGEIAPTHLRGALGTNLQLAIVIGILIAQVLGLESLLGTASLWPLLLGLTVLPALLQLVLLPFCPE
SPRYLYIIQNLGEPARKSLKRLTGWADVSGVLAELKDEKRLERERPLSLLQLLGSRTHRQPLIIAVVLQLSQQLSGIN
AVFYYSTSI FETAGVGQPAYATIGAGVVNTVFTLVSVLLVERAGRRTLHLLGLAGMCGCAILMTVALLLLERV PAMSYV
SIVAI FGFVAFFEIGPGPIPFVFAELFSQGRPAAMAVAGFSNWT SNFIIGMGFQYVAEAMGPYVFLFAVLLLGFFI
FTFLRVPETRGRTFDQISAAFHRTPSLLEQEVKPSIEPAKETTTNV
<seq007;prt/1;GLUT4 L489,490A mutant

<400> 6

Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
1 5 10 15

Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
20 25 30

Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
35 40 45

Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
 50 55 60

Gly Pro Glu Ile Asp Glu Gly Pro Ser Ser Ile Pro Pro Gly Thr Leu
 65 70 75 80

Thr Thr Leu Trp Ala Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met
 85 90 95

Ile Ser Ser Phe Leu Ile Gly Ile Ile Ser Gln Trp Leu Gly Arg Lys
 100 105 110

Arg Ala Met Leu Val Asn Asn Val Leu Ala Val Leu Gly Gly Ser Leu
 115 120 125

Met Gly Leu Ala Asn Ala Ala Ala Ser Tyr Glu Met Leu Ile Leu Gly
 130 135 140

Arg Phe Leu Ile Gly Ala Tyr Ser Gly Leu Thr Ser Gly Leu Val Pro
 145 150 155 160

Met Tyr Val Gly Glu Ile Ala Pro Thr His Leu Arg Gly Ala Leu Gly
 165 170 175

Thr Leu Asn Gln Leu Ala Ile Val Ile Gly Ile Leu Ile Ala Gln Val
 180 185 190

Leu Gly Leu Glu Ser Leu Leu Gly Thr Ala Ser Leu Trp Pro Leu Leu
 195 200 205

Leu Gly Leu Thr Val Leu Pro Ala Leu Leu Gln Leu Val Leu Leu Pro
 210 215 220

Phe Cys Pro Glu Ser Pro Arg Tyr Leu Tyr Ile Ile Gln Asn Leu Glu
 225 230 235 240

Gly Pro Ala Arg Lys Ser Leu Lys Arg Leu Thr Gly Trp Ala Asp Val
 245 250 255

Ser Gly Val Leu Ala Glu Leu Lys Asp Glu Lys Arg Lys Leu Glu Arg
 260 265 270

Glu Arg Pro Leu Ser Leu Leu Gln Leu Leu Gly Ser Arg Thr His Arg
 275 280 285

Gln Pro Leu Ile Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser
 290 295 300

Gly Ile Asn Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Thr Ala
 305 310 315 320

Gly Val Gly Gln Pro Ala Tyr Ala Thr Ile Gly Ala Gly Val Val Asn
 325 330 335

Thr Val Phe Thr Leu Val Ser Val Leu Leu Val Glu Arg Ala Gly Arg
 340 345 350

Arg Thr Leu His Leu Leu Gly Leu Ala Gly Met Cys Gly Cys Ala Ile
 355 360 365

Leu Met Thr Val Ala Leu Leu Leu Leu Glu Arg Val Pro Ala Met Ser
 370 375 380

Tyr Val Ser Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile
 385 390 395 400

Gly Pro Gly Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln
 405 410 415

Gly Pro Arg Pro Ala Ala Met Ala Val Ala Gly Phe Ser Asn Trp Thr
 420 425 430

Ser Asn Phe Ile Ile Gly Met Gly Phe Gln Tyr Val Ala Glu Ala Met
 435 440 445

Gly Pro Tyr Val Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe
 450 455 460

Ile Phe Thr Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp
 465 470 475 480

Gln Ile Ser Ala Ala Phe His Arg Thr Pro Ser Ala Ala Glu Gln Glu
 485 490 495

Val Lys Pro Ser Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu Asn Asp
 500 505 510

<210> 7
 <211> 521
 <212> PRT
 <213> HA tagged GLUT4 L489,490A mutant

<400> 7

Met Pro Ser Gly Phe Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
 1 5 10 15

15

Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
 20 25 30

Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
 35 40 45

Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
 50 55 60

Gly Pro Glu Ile Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Glu Gly
 65 70 75 80

Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser
 85 90 95

Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly
 100 105 110

Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn
 115 120 125

Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala
 130 135 140

Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr
 145 150 155 160

Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala
 165 170 175

Pro Thr His Leu Arg Gly Ala Leu Gly Thr Leu Asn Gln Leu Ala Ile
 180 185 190

Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly Leu Glu Ser Leu Leu
 195 200 205

Gly Thr Ala Ser Leu Trp Pro Leu Leu Leu Gly Leu Thr Val Leu Pro
 210 215 220

Ala Leu Leu Gln Leu Val Leu Leu Pro Phe Cys Pro Glu Ser Pro Arg
 225 230 235 240

Tyr Leu Tyr Ile Ile Gln Asn Leu Glu Gly Pro Ala Arg Lys Ser Leu
 245 250 255

Lys Arg Leu Thr Gly Trp Ala Asp Val Ser Gly Val Leu Ala Glu Leu

Lys	Asp	Glu	Lys	Arg	Lys	Leu	Glu	Arg	Glu	Arg	Pro	Leu	Ser	Leu	Leu
		275					280					285			
Gln	Leu	Leu	Gly	Ser	Arg	Thr	His	Arg	Gln	Pro	Leu	Ile	Ile	Ala	Val
	290					295					300				
Val	Leu	Gln	Leu	Ser	Gln	Gln	Leu	Ser	Gly	Ile	Asn	Ala	Val	Phe	Tyr
305					310					315					320
Tyr	Ser	Thr	Ser	Ile	Phe	Glu	Thr	Ala	Gly	Val	Gly	Gln	Pro	Ala	Tyr
				325					330					335	
Ala	Thr	Ile	Gly	Ala	Gly	Val	Val	Asn	Thr	Val	Phe	Thr	Leu	Val	Ser
			340					345					350		
Val	Leu	Leu	Val	Glu	Arg	Ala	Gly	Arg	Arg	Thr	Leu	His	Leu	Leu	Gly
		355					360					365			
Leu	Ala	Gly	Met	Cys	Gly	Cys	Ala	Ile	Leu	Met	Thr	Val	Ala	Leu	Leu
	370					375					380				
Leu	Leu	Glu	Arg	Val	Pro	Ala	Met	Ser	Tyr	Val	Ser	Ile	Val	Ala	Ile
385					390					395					400
Phe	Gly	Phe	Val	Ala	Phe	Phe	Glu	Ile	Gly	Pro	Gly	Pro	Ile	Pro	Trp
				405					410					415	
Phe	Ile	Val	Ala	Glu	Leu	Phe	Ser	Gln	Gly	Pro	Arg	Pro	Ala	Ala	Met
			420					425					430		
Ala	Val	Ala	Gly	Phe	Ser	Asn	Trp	Thr	Ser	Asn	Phe	Ile	Ile	Gly	Met
		435					440					445			
Gly	Phe	Gln	Tyr	Val	Ala	Glu	Ala	Met	Gly	Pro	Tyr	Val	Phe	Leu	Leu
	450					455					460				
Phe	Ala	Val	Leu	Leu	Leu	Gly	Phe	Phe	Ile	Phe	Thr	Phe	Leu	Arg	Val
465					470					475					480
Pro	Glu	Thr	Arg	Gly	Arg	Thr	Phe	Asp	Gln	Ile	Ser	Ala	Ala	Phe	His
				485					490					495	
Arg	Thr	Pro	Ser	Ala	Ala	Glu	Gln	Glu	Val	Lys	Pro	Ser	Thr	Glu	Leu
			500					505					510		

17

Glu Tyr Leu Gly Pro Asp Glu Asn Asp
 515 520

<210> 8
 <211> 512
 <212> PRT
 <213> GLUT4 F5A mutant
 <400> 8

Met Pro Ser Gly Ala Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
 1 5 10 15

Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
 20 25 30

Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
 35 40 45

Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
 50 55 60

Gly Pro Glu Ile Asp Glu Gly Pro Ser Ser Ile Pro Pro Gly Thr Leu
 65 70 75 80

Thr Thr Leu Trp Ala Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met
 85 90 95

Ile Ser Ser Phe Leu Ile Gly Ile Ile Ser Gln Trp Leu Gly Arg Lys
 100 105 110

Arg Ala Met Leu Val Asn Asn Val Leu Ala Val Leu Gly Gly Ser Leu
 115 120 125

Met Gly Leu Ala Asn Ala Ala Ala Ser Tyr Glu Met Leu Ile Leu Gly
 130 135 140

Arg Phe Leu Ile Gly Ala Tyr Ser Gly Leu Thr Ser Gly Leu Val Pro
 145 150 155 160

Met Tyr Val Gly Glu Ile Ala Pro Thr His Leu Arg Gly Ala Leu Gly
 165 170 175

Thr Leu Asn Gln Leu Ala Ile Val Ile Gly Ile Leu Ile Ala Gln Val
 180 185 190

Leu Gly Leu Glu Ser Leu Leu Gly Thr Ala Ser Leu Trp Pro Leu Leu
 195 200 205

Leu Gly Leu Thr Val Leu Pro Ala Leu Leu Gln Leu Val Leu Leu Pro
 210 215 220
 Phe Cys Pro Glu Ser Pro Arg Tyr Leu Tyr Ile Ile Gln Asn Leu Glu
 225 230 235 240
 Gly Pro Ala Arg Lys Ser Leu Lys Arg Leu Thr Gly Trp Ala Asp Val
 245 250 255
 Ser Gly Val Leu Ala Glu Leu Lys Asp Glu Lys Arg Lys Leu Glu Arg
 260 265 270
 Glu Arg Pro Leu Ser Leu Leu Gln Leu Leu Gly Ser Arg Thr His Arg
 275 280 285
 Gln Pro Leu Ile Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser
 290 295 300
 Gly Ile Asn Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Thr Ala
 305 310 315 320
 Gly Val Gly Gln Pro Ala Tyr Ala Thr Ile Gly Ala Gly Val Val Asn
 325 330 335
 Thr Val Phe Thr Leu Val Ser Val Leu Leu Val Glu Arg Ala Gly Arg
 340 345 350
 Arg Thr Leu His Leu Leu Gly Leu Ala Gly Met Cys Gly Cys Ala Ile
 355 360 365
 Leu Met Thr Val Ala Leu Leu Leu Leu Glu Arg Val Pro Ala Met Ser
 370 375 380
 Tyr Val Ser Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Ile
 385 390 395 400
 Gly Pro Gly Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln
 405 410 415
 Gly Pro Arg Pro Ala Ala Met Ala Val Ala Gly Phe Ser Asn Trp Thr
 420 425 430
 Ser Asn Phe Ile Ile Gly Met Gly Phe Gln Tyr Val Ala Glu Ala Met
 435 440 445
 Gly Pro Tyr Val Phe Leu Leu Phe Ala Val Leu Leu Leu Gly Phe Phe
 450 455 460

Ile Phe Thr Phe Leu Arg Val Pro Glu Thr Arg Gly Arg Thr Phe Asp
465 470 475 480

Gln Ile Ser Ala Ala Phe His Arg Thr Pro Ser Leu Leu Glu Gln Glu
485 490 495

Val Lys Pro Ser Thr Glu Leu Glu Tyr Leu Gly Pro Asp Glu Asn Asp
500 505 510

<210> 9
<211> 521
<212> PRT
<213> HA tagged GLUT4 F5A mutant

<400> 9

Met Pro Ser Gly Ala Gln Gln Ile Gly Ser Glu Asp Gly Glu Pro Pro
1 5 10 15

Gln Gln Arg Val Thr Gly Thr Leu Val Leu Ala Val Phe Ser Ala Val
20 25 30

Leu Gly Ser Leu Gln Phe Gly Tyr Asn Ile Gly Val Ile Asn Ala Pro
35 40 45

Gln Lys Val Ile Glu Gln Ser Tyr Asn Glu Thr Trp Leu Gly Arg Gln
50 55 60

Gly Pro Glu Ile Asp Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Glu Gly
65 70 75 80

Pro Ser Ser Ile Pro Pro Gly Thr Leu Thr Thr Leu Trp Ala Leu Ser
85 90 95

Val Ala Ile Phe Ser Val Gly Gly Met Ile Ser Ser Phe Leu Ile Gly
100 105 110

Ile Ile Ser Gln Trp Leu Gly Arg Lys Arg Ala Met Leu Val Asn Asn
115 120 125

Val Leu Ala Val Leu Gly Gly Ser Leu Met Gly Leu Ala Asn Ala Ala
130 135 140

Ala Ser Tyr Glu Met Leu Ile Leu Gly Arg Phe Leu Ile Gly Ala Tyr
145 150 155 160

Ser Gly Leu Thr Ser Gly Leu Val Pro Met Tyr Val Gly Glu Ile Ala
165 170 175

Pro Thr His Leu Arg Gly Ala Leu Gly Thr Leu Asn Gln Leu Ala Ile
 180 185 190

Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly Leu Glu Ser Leu Leu
 195 200 205

Gly Thr Ala Ser Leu Trp Pro Leu Leu Leu Gly Leu Thr Val Leu Pro
 210 215 220

Ala Leu Leu Gln Leu Val Leu Leu Pro Phe Cys Pro Glu Ser Pro Arg
 225 230 235 240

Tyr Leu Tyr Ile Ile Gln Asn Leu Glu Gly Pro Ala Arg Lys Ser Leu
 245 250 255

Lys Arg Leu Thr Gly Trp Ala Asp Val Ser Gly Val Leu Ala Glu Leu
 260 265 270

Lys Asp Glu Lys Arg Lys Leu Glu Arg Glu Arg Pro Leu Ser Leu Leu
 275 280 285

Gln Leu Leu Gly Ser Arg Thr His Arg Gln Pro Leu Ile Ile Ala Val
 290 295 300

Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr
 305 310 315 320

Tyr Ser Thr Ser Ile Phe Glu Thr Ala Gly Val Gly Gln Pro Ala Tyr
 325 330 335

Ala Thr Ile Gly Ala Gly Val Val Asn Thr Val Phe Thr Leu Val Ser
 340 345 350

Val Leu Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Leu Leu Gly
 355 360 365

Leu Ala Gly Met Cys Gly Cys Ala Ile Leu Met Thr Val Ala Leu Leu
 370 375 380

Leu Leu Glu Arg Val Pro Ala Met Ser Tyr Val Ser Ile Val Ala Ile
 385 390 395 400

Phe Gly Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro Ile Pro Trp
 405 410 415

Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Met
 420 425 430

Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe Ile Ile Gly Met
 435 440 445

Gly Phe Gln Tyr Val Ala Glu Ala Met Gly Pro Tyr Val Phe Leu Leu
 450 455 460

Phe Ala Val Leu Leu Leu Gly Phe Phe Ile Phe Thr Phe Leu Arg Val
 465 470 475 480

Pro Glu Thr Arg Gly Arg Thr Phe Asp Gln Ile Ser Ala Ala Phe His
 485 490 495

Arg Thr Pro Ser Leu Leu Glu Gln Glu Val Lys Pro Ser Thr Glu Leu
 500 505 510

Glu Tyr Leu Gly Pro Asp Glu Asn Asp
 515 520

<210> 10
 <211> 2856
 <212> DNA
 <213> GLUT1

<220>
 <221> CDS
 <222> (180)..(1658)
 <223>

<400> 10
 tagtcgctggg tccccgagtg agcacgccag ggagcaggag accaaacgac gggggtcggg 60
 gtcagagtcg cagtgggagt.ccccgaccg gagcacgagc ctgagcggga gagcgccgct 120
 cgcacgcccg tcgccaccg cgtaccgggc gcagccagag ccaccagcgc agcgtgccc 179
 atg gag ccc agc agc aag aag ctg acg ggt cgc ctc atg ctg gct gtg 227
 Met Glu Pro Ser Ser Lys Lys Leu Thr Gly Arg Leu Met Leu Ala Val
 1 5 10 15
 gga gga gca gtg ctt ggc tcc ctg cag ttt ggc tac aac act gga gtc 275
 Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val
 20 25 30
 atc aat gcc ccc cag aag gtg atc gag gag ttc tac aac cag aca tgg 323
 Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp
 35 40 45
 gtc cac cgc tat ggg gag agc atc ctg ccc acc acg ctc acc acg ctc 371
 Val His Arg Tyr Gly Glu Ser Ile Leu Pro Thr Thr Leu Thr Thr Leu
 50 55 60
 tgg tcc ctc tca gtg gcc atc ttt tct gtt ggg ggc atg att ggc tcc 419
 Trp Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser
 65 70 75 80

ttc tct gtg ggc ctt ttc gtt aac cgc ttt ggc cgg cgg aat tca atg Phe Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met 85 90 95	467
ctg atg atg aac ctg ctg gcc ttc gtg tcc gcc gtg ctc atg ggc ttc Leu Met Met Asn Leu Leu Ala Phe Val Ser Ala Val Leu Met Gly Phe 100 105 110	515
tcg aaa ctg ggc aag tcc ttt gag atg ctg atc ctg ggc cgc ttc atc Ser Lys Leu Gly Lys Ser Phe Glu Met Leu Ile Leu Gly Arg Phe Ile 115 120 125	563
atc ggt gtg tac tgc ggc ctg acc aca gcc ttc gtg ccc atg tat gtg Ile Gly Val Tyr Cys Gly Leu Thr Thr Gly Phe Val Pro Met Tyr Val 130 135 140	611
ggt gaa gtg tca ccc aca gcc ttt cgt ggg gcc ctg ggc acc ctg cac Gly Glu Val Ser Pro Thr Ala Phe Arg Gly Ala Leu Gly Thr Leu His 145 150 155 160	659
cag ctg ggc atc gtc gtc ggc atc ctc atc gcc cag gtg ttc ggc ctg Gln Leu Gly Ile Val Val Gly Ile Leu Ile Ala Gln Val Phe Gly Leu 165 170 175	707
gac tcc atc atg ggc aac aag gac ctg tgg ccc ctg ctg ctg agc atc Asp Ser Ile Met Gly Asn Lys Asp Leu Trp Pro Leu Leu Leu Ser Ile 180 185 190	755
atc ttc atc ccg gcc ctg ctg cag tgc atc gtg ctg ccc ttc tgc ccc Ile Phe Ile Pro Ala Leu Leu Gln Cys Ile Val Leu Pro Phe Cys Pro 195 200 205	803
gag agt ccc cgc ttc ctg ctc atc aac cgc aac gag gag aac cgg gcc Glu Ser Pro Arg Phe Leu Leu Ile Asn Arg Asn Glu Glu Asn Arg Ala 210 215 220	851
aag agt gtg cta aag aag ctg cgc ggg aca gct gac gtg acc cat gac Lys Ser Val Leu Lys Lys Leu Arg Gly Thr Ala Asp Val Thr His Asp 225 230 235 240	899
ctg cag gag atg aag gaa gag agt cgg cag atg atg cgg gag aag aag Leu Gln Glu Met Lys Glu Glu Ser Arg Gln Met Met Arg Glu Lys Lys 245 250 255	947
gtc acc atc ctg gag ctg ttc cgc tcc ccc gcc tac cgc cag ccc atc Val Thr Ile Leu Glu Leu Phe Arg Ser Pro Ala Tyr Arg Gln Pro Ile 260 265 270	995
ctc atc gct gtg gtg ctg cag ctg tcc cag cag ctg tct ggc atc aac Leu Ile Ala Val Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn 275 280 285	1043
gct gtc ttc tat tac tcc acg agc atc ttc gag aag gcg ggg gtg cag Ala Val Phe Tyr Tyr Ser Thr Ser Ile Phe Glu Lys Ala Gly Val Gln 290 295 300	1091
cag cct gtg tat gcc acc att ggc tcc ggt atc gtc aac acg gcc ttc Gln Pro Val Tyr Ala Thr Ile Gly Ser Gly Ile Val Asn Thr Ala Phe 305 310 315 320	1139
act gtc gtg tcg ctg ttt gtg gtg gag cga gca ggc cgg cgg acc ctg Thr Val Val Ser Leu Phe Val Val Glu Arg Ala Gly Arg Arg Thr Leu 325 330 335	1187

cac ctc ata ggc ctc gct ggc atg gcg ggt tgt gcc ata ctc atg acc His Leu Ile Gly Leu Ala Gly Met Ala Gly Cys Ala Ile Leu Met Thr 340 345 350	1235
atc gcg cta gca ctg ctg gag cag cta ccc tgg atg tcc tat ctg agc Ile Ala Leu Ala Leu Leu Glu Gln Leu Pro Trp Met Ser Tyr Leu Ser 355 360 365	1283
atc gtg gcc atc ttt ggc ttt gtg gcc ttc ttt gaa gtg ggt cct ggc Ile Val Ala Ile Phe Gly Phe Val Ala Phe Phe Glu Val Gly Pro Gly 370 375 380	1331
ccc atc cca tgg ttc atc gtg gct gaa ctc ttc agc cag ggt cca cgt Pro Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg 385 390 395 400	1379
cca gct gcc att gcc gtt gca ggc ttc tcc aac tgg acc tca aat ttc Pro Ala Ala Ile Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe 405 410 415	1427
att gtg ggc atg tgc ttc cag tat gtg gag caa ctg tgt ggt ccc tac Ile Val Gly Met Cys Phe Gln Tyr Val Glu Gln Leu Cys Gly Pro Tyr 420 425 430	1475
gtc ttc atc atc ttc act gtg ctc ctg gtt ctg ttc ttc atc ttc acc Val Phe Ile Ile Phe Thr Val Leu Leu Val Leu Phe Phe Ile Phe Thr 435 440 445	1523
tac ttc aaa gtt cct gag act aaa ggc cgg acc ttc gat gag atc gct Tyr Phe Lys Val Pro Glu Thr Lys Gly Arg Thr Phe Asp Glu Ile Ala 450 455 460	1571
tcc ggc ttc cgg cag ggg gga gcc agc caa agt gat aag aca ccc gag Ser Gly Phe Arg Gln Gly Gly Ala Ser Gln Ser Asp Lys Thr Pro Glu 465 470 475 480	1619
gag ctg ttc cat ccc ctg ggg gct gat tcc caa gtg tga gtcgccccag Glu Leu Phe His Pro Leu Gly Ala Asp Ser Gln Val 485 490	1668
atcaccagcc cggcctgctc ccagcagccc taaggatctc tcaggagcac aggcagctgg	1728
atgagacttc caaacctgac agatgtcagc cgagccgggc ctggggctcc tttctccagc	1788
cagcaatgat gtccagaaga atattcagga cttaacggct ccaggatttt aacaaaagca	1848
agactgttgc tcaaattctat tcagacaagc aacaggtttt ataatttttt tattactgat	1908
tttgttattt ttatatcagc ctgagtctcc tgtgccaca tcccaggctt caccctgaat	1968
ggttccatgc ctgagggtgg agactaagcc ctgtcgagac acttgccttc ttcacccagc	2028
taatctgtag ggctggacct atgtcctaag gacacactaa tcgaactatg aactacaaaag	2088
cttctatccc aggaggtggc tatggccacc cgttctgctg gcctggatct cccactcta	2148
ggggtcaggc tccattagga ttgcccctt cccatctctt cctaccaaac cactcaaatt	2208
aatctttctt tacctgagac cagttgggag cactggagtg cagggaggag aggggaaggg	2268
ccagtctggg ctgccgggtt ctagtctcct ttgcaactgag ggccacacta ttacatgag	2328

24

aagagggcct gtgggagcct gcaaactcac tgctcaagaa gacatggaga ctctgcct 2388
gttgtgtata gatgcaagat atttatatat atttttggtt gtcaatatta aatacagaca 2448
ctaagttata gtatatctgg acaagccaac ttgtaaatac accacctcac tcctgttact 2508
tacctaaca gataaaatg gctgggtttt agaaacatgg ttttgaaatg cttgtggatt 2568
gagggtagga ggtttgatg ggagtggagac agaagtaagt ggggttgcaa ccactgcaac 2628
ggcttagact tcgactcagg atccagtccc ttacacgtac ctctcatcag tgcctcttg 2688
ctcaaaaatc tgtttgatcc ctgttaccca gagaatatat acattcttta tcttgacatt 2748
caaggcattt ctatcacata tttgatagtt ggtgttcaaa aaaacactag ttttgtgcca 2808
gccgtgatgc tcaggcttga aatcgcattha ttttgaatgt gaaggga 2856

<210> 11
<211> 492
<212> PRT
<213> GLUT1

<400> 11

Met Glu Pro Ser Ser Lys Lys Leu Thr Gly Arg Leu Met Leu Ala Val
1 5 10 15

Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val
20 25 30

Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp
35 40 45

Val His Arg Tyr Gly Glu Ser Ile Leu Pro Thr Thr Leu Thr Thr Leu
50 55 60

Trp Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser
65 70 75 80

Phe Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met
85 90 95

Leu Met Met Asn Leu Leu Ala Phe Val Ser Ala Val Leu Met Gly Phe
100 105 110

Ser Lys Leu Gly Lys Ser Phe Glu Met Leu Ile Leu Gly Arg Phe Ile
115 120 125

Ile Gly Val Tyr Cys Gly Leu Thr Thr Gly Phe Val Pro Met Tyr Val
130 135 140

Gly Glu Val Ser Pro Thr Ala Phe Arg Gly Ala Leu Gly Thr Leu His

25

145		150		155		160
Gln Leu Gly Ile Val	Val Gly Ile Leu Ile	Ala Gln Val Phe Gly Leu				
	165		170			175
Asp Ser Ile Met Gly	Asn Lys Asp Leu Trp	Pro Leu Leu Leu Ser Ile				
	180	185			190	
Ile Phe Ile Pro Ala	Leu Leu Gln Cys Ile	Val Leu Pro Phe Cys Pro				
	195	200		205		
Glu Ser Pro Arg Phe	Leu Leu Ile Asn Arg	Asn Glu Glu Asn Arg Ala				
	210	215		220		
Lys Ser Val Leu Lys	Lys Leu Arg Gly Thr	Ala Asp Val Thr His Asp				
225		230		235		240
Leu Gln Glu Met Lys	Glu Glu Ser Arg Gln	Met Met Arg Glu Lys Lys				
	245	250			255	
Val Thr Ile Leu Glu	Leu Phe Arg Ser Pro	Ala Tyr Arg Gln Pro Ile				
	260	265			270	
Leu Ile Ala Val Val	Leu Gln Leu Ser Gln	Gln Leu Ser Gly Ile Asn				
	275	280		285		
Ala Val Phe Tyr Tyr	Ser Thr Ser Ile Phe	Glu Lys Ala Gly Val Gln				
	290	295		300		
Gln Pro Val Tyr Ala	Thr Ile Gly Ser Gly	Ile Val Asn Thr Ala Phe				
305		310		315		320
Thr Val Val Ser Leu	Phe Val Val Glu Arg	Ala Gly Arg Arg Thr Leu				
	325	330			335	
His Leu Ile Gly Leu	Ala Gly Met Ala Gly	Cys Ala Ile Leu Met Thr				
	340	345			350	
Ile Ala Leu Ala Leu	Leu Glu Gln Leu Pro	Trp Met Ser Tyr Leu Ser				
	355	360		365		
Ile Val Ala Ile Phe	Gly Phe Val Ala Phe	Phe Glu Val Gly Pro Gly				
	370	375		380		
Pro Ile Pro Trp Phe	Ile Val Ala Glu Leu	Phe Ser Gln Gly Pro Arg				
385		390		395		400

Pro Ala Ala Ile Ala Val Ala Gly Phe Ser Asn Trp Thr Ser Asn Phe
 405 410 415

Ile Val Gly Met Cys Phe Gln Tyr Val Glu Gln Leu Cys Gly Pro Tyr
 420 425 430

Val Phe Ile Ile Phe Thr Val Leu Leu Val Leu Phe Phe Ile Phe Thr
 435 440 445

Tyr Phe Lys Val Pro Glu Thr Lys Gly Arg Thr Phe Asp Glu Ile Ala
 450 455 460

Ser Gly Phe Arg Gln Gly Gly Ala Ser Gln Ser Asp Lys Thr Pro Glu
 465 470 475 480

Glu Leu Phe His Pro Leu Gly Ala Asp Ser Gln Val
 485 490

<210> 12
 <211> 1506
 <212> DNA
 <213> HA tagged GLUT1

<220>
 <221> CDS
 <222> (1)..(1506)
 <223>

<400> 12
 atg gag ccc agc agc aag aag ctg acg ggt cgc ctc atg ctg gct gtg 48
 Met Glu Pro Ser Ser Lys Lys Leu Thr Gly Arg Leu Met Leu Ala Val
 1 5 10 15
 gga gga gca gtg ctt ggc tcc ctg cag ttt ggc tac aac act gga gtc 96
 Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val
 20 25 30
 atc aat gcc ccc cag aag gtg atc gag gag ttc tac aac cag aca tgg 144
 Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp
 35 40 45
 gtc cac cgc tat ggg gag agc atc tac cca tac gac gtc cca gac tac 192
 Val His Arg Tyr Gly Glu Ser Ile Tyr Pro Tyr Asp Val Pro Asp Tyr
 50 55 60
 gct ctg ccc acc acg ctc acc acg ctc tgg tcc ctc tca gtg gcc atc 240
 Ala Leu Pro Thr Thr Leu Thr Thr Leu Trp Ser Leu Ser Val Ala Ile
 65 70 75 80
 ttt tct gtt ggg ggc atg att ggc tcc ttc tct gtg ggc ctt ttc gtt 288
 Phe Ser Val Gly Gly Met Ile Gly Ser Phe Ser Val Gly Leu Phe Val
 85 90 95
 aac cgc ttt ggc cgg cgg aat tca atg ctg atg atg aac ctg ctg gcc 336
 Asn Arg Phe Gly Arg Arg Asn Ser Met Leu Met Met Asn Leu Leu Ala
 100 105 110

ttc gtg tcc gcc gtg ctc atg ggc ttc tcg aaa ctg ggc aag tcc ttt Phe Val Ser Ala Val Leu Met Gly Phe Ser Lys Leu Gly Lys Ser Phe 115 120 125	384
gag atg ctg atc ctg ggc cgc ttc atc atc ggt gtg tac tgc ggc ctg Glu Met Leu Ile Leu Gly Arg Phe Ile Ile Gly Val Tyr Cys Gly Leu 130 135 140	432
acc aca ggc ttc gtg ccc atg tat gtg ggt gaa gtg tca ccc aca gcc Thr Thr Gly Phe Val Pro Met Tyr Val Gly Glu Val Ser Pro Thr Ala 145 150 155 160	480
ttt cgt ggg gcc ctg ggc acc ctg cac cag ctg ggc atc gtc gtc ggc Phe Arg Gly Ala Leu Gly Thr Leu His Gln Leu Gly Ile Val Val Gly 165 170 175	528
atc ctc atc gcc cag gtg ttc ggc ctg gac tcc atc atg ggc aac aag Ile Leu Ile Ala Gln Val Phe Gly Leu Asp Ser Ile Met Gly Asn Lys 180 185 190	576
gac ctg tgg ccc ctg ctg ctg agc atc atc ttc atc ccg gcc ctg ctg Asp Leu Trp Pro Leu Leu Leu Ser Ile Ile Phe Ile Pro Ala Leu Leu 195 200 205	624
cag tgc atc gtg ctg ccc ttc tgc ccc gag agt ccc cgc ttc ctg ctc Gln Cys Ile Val Leu Pro Phe Cys Pro Glu Ser Pro Arg Phe Leu Leu 210 215 220	672
atc aac cgc aac gag gag aac cgg gcc aag agt gtg cta aag aag ctg Ile Asn Arg Asn Glu Glu Asn Arg Ala Lys Ser Val Leu Lys Lys Leu 225 230 235 240	720
cgc ggg aca gct gac gtg acc cat gac ctg cag gag atg aag gaa gag Arg Gly Thr Ala Asp Val Thr His Asp Leu Gln Glu Met Lys Glu Glu 245 250 255	768
agt cgg cag atg atg cgg gag aag aag gtc acc atc ctg gag ctg ttc Ser Arg Gln Met Met Arg Glu Lys Lys Val Thr Ile Leu Glu Leu Phe 260 265 270	816
cgc tcc ccc gcc tac cgc cag ccc atc ctc atc gct gtg gtg ctg cag Arg Ser Pro Ala Tyr Arg Gln Pro Ile Leu Ile Ala Val Val Leu Gln 275 280 285	864
ctg tcc cag cag ctg tct ggc atc aac gct gtc ttc tat tac tcc acg Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr Tyr Ser Thr 290 295 300	912
agc atc ttc gag aag gcg ggg gtg cag cag cct gtg tat gcc acc att Ser Ile Phe Glu Lys Ala Gly Val Gln Gln Pro Val Tyr Ala Thr Ile 305 310 315 320	960
ggc tcc ggt atc gtc aac acg gcc ttc act gtc gtg tcg ctg ttt gtg Gly Ser Gly Ile Val Asn Thr Ala Phe Thr Val Val Ser Leu Phe Val 325 330 335	1008
gtg gag cga gca ggc cgg cgg acc ctg cac ctc ata ggc ctc gct ggc Val Glu Arg Ala Gly Arg Arg Thr Leu His Leu Ile Gly Leu Ala Gly 340 345 350	1056
atg gcg ggt tgt gcc ata ctc atg acc atc gcg cta gca ctg ctg gag Met Ala Gly Cys Ala Ile Leu Met Thr Ile Ala Leu Ala Leu Leu Glu 355 360 365	1104

cag cta ccc tgg atg tcc tat ctg agc atc gtg gcc atc ttt ggc ttt 1152
 Gln Leu Pro Trp Met Ser Tyr Leu Ser Ile Val Ala Ile Phe Gly Phe
 370 375 380
 gtg gcc ttc ttt gaa gtg ggt cct ggc ccc atc cca tgg ttc atc gtg 1200
 Val Ala Phe Phe Glu Val Gly Pro Gly Pro Ile Pro Trp Phe Ile Val
 385 390 395 400
 gct gaa ctc ttc agc cag ggt cca cgt cca gct gcc att gcc gtt gca 1248
 Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Ile Ala Val Ala
 405 410 415
 ggc ttc tcc aac tgg acc tca aat ttc att gtg ggc atg tgc ttc cag 1296
 Gly Phe Ser Asn Trp Thr Ser Asn Phe Ile Val Gly Met Cys Phe Gln
 420 425 430
 tat gtg gag caa ctg tgt ggt ccc tac gtc ttc atc atc ttc act gtg 1344
 Tyr Val Glu Gln Leu Cys Gly Pro Tyr Val Phe Ile Ile Phe Thr Val
 435 440 445
 ctc ctg gtt ctg ttc ttc atc ttc acc tac ttc aaa gtt cct gag act 1392
 Leu Leu Val Leu Phe Phe Ile Phe Thr Tyr Phe Lys Val Pro Glu Thr
 450 455 460
 aaa ggc cgg acc ttc gat gag atc gct tcc ggc ttc cgg cag ggg gga 1440
 Lys Gly Arg Thr Phe Asp Glu Ile Ala Ser Gly Phe Arg Gln Gly Gly
 465 470 475 480
 gcc agc caa agt gat aag aca ccc gag gag ctg ttc cat ccc ctg ggg 1488
 Ala Ser Gln Ser Asp Lys Thr Pro Glu Glu Leu Phe His Pro Leu Gly
 485 490 495
 gct gat tcc caa gtg tga 1506
 Ala Asp Ser Gln Val
 500

<210> 13
 <211> 501
 <212> PRT
 <213> HA tagged GLUT1

<400> 13

Met Glu Pro Ser Ser Lys Lys Leu Thr Gly Arg Leu Met Leu Ala Val
 1 5 10 15
 Gly Gly Ala Val Leu Gly Ser Leu Gln Phe Gly Tyr Asn Thr Gly Val
 20 25 30
 Ile Asn Ala Pro Gln Lys Val Ile Glu Glu Phe Tyr Asn Gln Thr Trp
 35 40 45
 Val His Arg Tyr Gly Glu Ser Ile Tyr Pro Tyr Asp Val Pro Asp Tyr
 50 55 60
 Ala Leu Pro Thr Thr Leu Thr Thr Leu Trp Ser Leu Ser Val Ala Ile
 65 70 75 80

Phe Ser Val Gly Gly Met Ile Gly Ser Phe Ser Val Gly Leu Phe Val
 85 90 95

Asn Arg Phe Gly Arg Arg Asn Ser Met Leu Met Met Asn Leu Leu Ala
 100 105 110

Phe Val Ser Ala Val Leu Met Gly Phe Ser Lys Leu Gly Lys Ser Phe
 115 120 125

Glu Met Leu Ile Leu Gly Arg Phe Ile Ile Gly Val Tyr Cys Gly Leu
 130 135 140

Thr Thr Gly Phe Val Pro Met Tyr Val Gly Glu Val Ser Pro Thr Ala
 145 150 155 160

Phe Arg Gly Ala Leu Gly Thr Leu His Gln Leu Gly Ile Val Val Gly
 165 170 175

Ile Leu Ile Ala Gln Val Phe Gly Leu Asp Ser Ile Met Gly Asn Lys
 180 185 190

Asp Leu Trp Pro Leu Leu Leu Ser Ile Ile Phe Ile Pro Ala Leu Leu
 195 200 205

Gln Cys Ile Val Leu Pro Phe Cys Pro Glu Ser Pro Arg Phe Leu Leu
 210 215 220

Ile Asn Arg Asn Glu Glu Asn Arg Ala Lys Ser Val Leu Lys Lys Leu
 225 230 235 240

Arg Gly Thr Ala Asp Val Thr His Asp Leu Gln Glu Met Lys Glu Glu
 245 250 255

Ser Arg Gln Met Met Arg Glu Lys Lys Val Thr Ile Leu Glu Leu Phe
 260 265 270

Arg Ser Pro Ala Tyr Arg Gln Pro Ile Leu Ile Ala Val Val Leu Gln
 275 280 285

Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr Tyr Ser Thr
 290 295 300

Ser Ile Phe Glu Lys Ala Gly Val Gln Gln Pro Val Tyr Ala Thr Ile
 305 310 315 320

Gly Ser Gly Ile Val Asn Thr Ala Phe Thr Val Val Ser Leu Phe Val

30

325 330 335
 Val Glu Arg Ala Gly Arg Arg Thr Leu His Leu Ile Gly Leu Ala Gly
 340 345 350
 Met Ala Gly Cys Ala Ile Leu Met Thr Ile Ala Leu Ala Leu Leu Glu
 355 360 365
 Gln Leu Pro Trp Met Ser Tyr Leu Ser Ile Val Ala Ile Phe Gly Phe
 370 375 380
 Val Ala Phe Phe Glu Val Gly Pro Gly Pro Ile Pro Trp Phe Ile Val
 385 390 395 400
 Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Ile Ala Val Ala
 405 410 415
 Gly Phe Ser Asn Trp Thr Ser Asn Phe Ile Val Gly Met Cys Phe Gln
 420 425 430
 Tyr Val Glu Gln Leu Cys Gly Pro Tyr Val Phe Ile Ile Phe Thr Val
 435 440 445
 Leu Leu Val Leu Phe Phe Ile Phe Thr Tyr Phe Lys Val Pro Glu Thr
 450 455 460
 Lys Gly Arg Thr Phe Asp Glu Ile Ala Ser Gly Phe Arg Gln Gly Gly
 465 470 475 480
 Ala Ser Gln Ser Asp Lys Thr Pro Glu Glu Leu Phe His Pro Leu Gly
 485 490 495
 Ala Asp Ser Gln Val
 500

<210> 14
 <211> 9
 <212> PRT
 <213> HA epitope

<400> 14

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> 15
 <211> 14
 <212> PRT
 <213> Simian Virus 5 epitope (SV5)

<400> 15

Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly Leu Asp Ser Thr
1 5 10

<210> 16

<211> 6

<212> PRT

<213> hexa-his

<400> 16

His His His His His His
1 5

<210> 17

<211> 10

<212> PRT

<213> c-myc epitope

<400> 17

Phe Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 18

<211> 9

<212> PRT

<213> FLAG epitope

<400> 18

Asp Tyr Lys Asp Asp Asp Asp Lys Cys
1 5

<210> 19

<211> 9

<212> PRT

<213> Alternative FLAG epitope

<400> 19

Met Asp Phe Lys Asp Asp Asp Asp Lys
1 5

<210> 20

<211> 9

<212> PRT

<213> Alternative FLAG epitope

<400> 20

Met Asp Tyr Lys Ala Phe Asp Asn Leu
1 5

<210> 21

<211> 223

32

<212> PRT

<213> glutathione-S-transferase

<400> 21

Met Ala Lys Leu Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val
 1 5 10 15

Gln Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
 20 25 30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe
 35 40 45

Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp
 50 55 60

Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys
 65 70 75 80

His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met
 85 90 95

Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala
 100 105 110

Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu
 115 120 125

Pro Glu Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr
 130 135 140

Leu Asn Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala
 145 150 155 160

Leu Asp Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro
 165 170 175

Lys Leu Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp
 180 185 190

Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp
 195 200 205

Gln Ala Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu
 210 215 220

<210> 22

<211> 488

<212> PRT

<213> maltose binding protein

<400> 22

Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys
 1 5 10 15

Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
 20 25 30

Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45

Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60

His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80

Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95

Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110

Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125

Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140

Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175

Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190

Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205

Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220

Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240

Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270

Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285

Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300

Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320

Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335

Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350

Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365

Ser Ser Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Leu Gly Ile
 370 375 380

Asp Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala Met Asp Pro Glu Phe
 385 390 395 400

Lys Gly Leu Arg Arg Arg Ala Gln Leu Val Arg Pro Leu Ser Asn Leu
 405 410 415

Glu Pro Ala Val Ser Arg His Ala Val Pro Ser Leu Ala Leu Ala Val
 420 425 430

Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu Asn
 435 440 445

Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu
 450 455 460

Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu
 465 470 475 480

Trp Gln Leu Gly Cys Phe Gly Gly

35

485

<210> 23
 <211> 168
 <212> PRT
 <213> GAL4

<400> 23

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
 1 5 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
 85 90 95

Phe Val Gln Asp Asn Val Asn Lys Asp Ala Val Thr Asp Arg Leu Ala
 100 105 110

Ser Val Glu Thr Asp Met Pro Leu Thr Leu Arg Gln His Arg Ile Ser
 115 120 125

Ala Thr Ser Ser Ser Glu Glu Ser Ser Asn Lys Gly Gln Arg Gln Leu
 130 135 140

Thr Val Ser Pro Glu Phe Pro Gly Ile Arg Arg Leu Asp Ala Leu Ile
 145 150 155 160

Ser Ser Arg Ala Ala Ala Gly Thr
 165

<210> 24
 <211> 1045
 <212> PRT
 <213> beta-galactosidase

<400> 24

Met Ser Phe Thr Leu Thr Asn Lys Asn Val Ile Phe Val Ala Gly Leu
 1 5 10 15

Gly Gly Ile Gly Leu Asp Thr Ser Lys Glu Leu Leu Lys Arg Asp Pro
 20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
 35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
 50 55 60

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
 65 70 75 80

Glu Trp Arg Phe Ala Trp Phe Pro Ala Pro Glu Ala Val Pro Glu Ser
 85 90 95

Trp Leu Glu Cys Asp Leu Pro Glu Ala Asp Thr Val Val Val Pro Ser
 100 105 110

Asn Trp Gln Met His Gly Tyr Asp Ala Pro Ile Tyr Thr Asn Val Thr
 115 120 125

Tyr Pro Ile Thr Val Asn Pro Pro Phe Val Pro Thr Glu Asn Pro Thr
 130 135 140

Gly Cys Tyr Ser Leu Thr Phe Asn Val Asp Glu Ser Trp Leu Gln Glu
 145 150 155 160

Gly Gln Thr Arg Ile Ile Phe Asp Gly Val Asn Ser Ala Phe His Leu
 165 170 175

Trp Cys Asn Gly Arg Trp Val Gly Tyr Gly Gln Asp Ser Arg Leu Pro
 180 185 190

Ser Glu Phe Asp Leu Ser Ala Phe Leu Arg Ala Gly Glu Asn Arg Leu
 195 200 205

Ala Val Met Val Leu Arg Trp Ser Asp Gly Ser Tyr Leu Glu Asp Gln
 210 215 220

Asp Met Trp Arg Met Ser Gly Ile Phe Arg Asp Val Ser Leu Leu His
 225 230 235 240

Lys Pro Thr Thr Gln Ile Ser Asp Phe His Val Ala Thr Arg Phe Asn
 245 250 255

Asp Asp Phe Ser Arg Ala Val Leu Glu Ala Glu Val Gln Met Cys Gly

260	265	270
Glu Leu Arg Asp Tyr Leu Arg Val Thr Val Ser Leu Trp Gln Gly Glu		
275	280	285
Thr Gln Val Ala Ser Gly Thr Ala Pro Phe Gly Gly Glu Ile Ile Asp		
290	295	300
Glu Arg Gly Gly Tyr Ala Asp Arg Val Thr Leu Arg Leu Asn Val Glu		
305	310	315
Asn Pro Lys Leu Trp Ser Ala Glu Ile Pro Asn Leu Tyr Arg Ala Val		
325	330	335
Val Glu Leu His Thr Ala Asp Gly Thr Leu Ile Glu Ala Glu Ala Cys		
340	345	350
Asp Val Gly Phe Arg Glu Val Arg Ile Glu Asn Gly Leu Leu Leu Leu		
355	360	365
Asn Gly Lys Pro Leu Leu Ile Arg Gly Val Asn Arg His Glu His His		
370	375	380
Pro Leu His Gly Gln Val Met Asp Glu Gln Thr Met Val Gln Asp Ile		
385	390	395
Leu Leu Met Lys Gln Asn Asn Phe Asn Ala Val Arg Cys Ser His Tyr		
405	410	415
Pro Asn His Pro Leu Trp Tyr Thr Leu Cys Asp Arg Tyr Gly Leu Tyr		
420	425	430
Val Val Asp Glu Ala Asn Ile Glu Thr His Gly Met Val Pro Met Asn		
435	440	445
Arg Leu Thr Asp Asp Pro Arg Trp Leu Pro Ala Met Ser Glu Arg Val		
450	455	460
Thr Arg Met Val Gln Arg Asp Arg Asn His Pro Ser Val Ile Ile Trp		
465	470	475
Ser Leu Gly Asn Glu Ser Gly His Gly Ala Asn His Asp Ala Leu Tyr		
485	490	495
Arg Trp Ile Lys Ser Val Asp Pro Ser Arg Pro Val Gln Tyr Glu Gly		
500	505	510

Gly Gly Ala Asp Thr Thr Ala Thr Asp Ile Ile Cys Pro Met Tyr Ala
 515 520 525

Arg Val Asp Glu Asp Gln Pro Phe Pro Ala Val Pro Lys Trp Ser Ile
 530 535 540

Lys Lys Trp Leu Ser Leu Pro Gly Glu Thr Arg Pro Leu Ile Leu Cys
 545 550 555 560

Glu Tyr Ala His Ala Met Gly Asn Ser Leu Gly Gly Phe Ala Lys Tyr
 565 570 575

Trp Gln Ala Phe Arg Gln Tyr Pro Arg Leu Gln Gly Gly Phe Val Trp
 580 585 590

Asp Trp Val Asp Gln Ser Leu Ile Lys Tyr Asp Glu Asn Gly Asn Pro
 595 600 605

Trp Ser Ala Tyr Gly Gly Asp Phe Gly Asp Thr Pro Asn Asp Arg Gln
 610 615 620

Phe Cys Met Asn Gly Leu Val Phe Ala Asp Arg Thr Pro His Pro Ala
 625 630 635 640

Leu Thr Glu Ala Lys His Gln Gln Gln Phe Phe Gln Phe Arg Leu Ser
 645 650 655

Gly Gln Thr Ile Glu Val Thr Ser Glu Tyr Leu Phe Arg His Ser Asp
 660 665 670

Asn Glu Leu Leu His Trp Met Val Ala Leu Asp Gly Lys Pro Leu Ala
 675 680 685

Ser Gly Glu Val Pro Leu Asp Val Ala Pro Gln Gly Lys Gln Leu Ile
 690 695 700

Glu Leu Pro Glu Leu Pro Gln Pro Glu Ser Ala Gly Gln Leu Trp Leu
 705 710 715 720

Thr Val Arg Val Val Gln Pro Asn Ala Thr Ala Trp Ser Glu Ala Gly
 725 730 735

His Ile Ser Ala Trp Gln Gln Trp Arg Leu Ala Glu Asn Leu Ser Val
 740 745 750

Thr Leu Pro Ala Ala Ser His Ala Ile Pro His Leu Thr Thr Ser Glu
 755 760 765

Met Asp Phe Cys Ile Glu Leu Gly Asn Lys Arg Trp Gln Phe Asn Arg
 770 775 780

Gln Ser Gly Phe Leu Ser Gln Met Trp Ile Gly Asp Lys Lys Gln Leu
 785 790 795 800

Leu Thr Pro Leu Arg Asp Gln Phe Thr Arg Ala Pro Leu Asp Asn Asp
 805 810 815

Ile Gly Val Ser Glu Ala Thr Arg Ile Asp Pro Asn Ala Trp Val Glu
 820 825 830

Arg Trp Lys Ala Ala Gly His Tyr Gln Ala Glu Ala Ala Leu Leu Gln
 835 840 845

Cys Thr Ala Asp Thr Leu Ala Asp Ala Val Leu Ile Thr Thr Ala His
 850 855 860

Ala Trp Gln His Gln Gly Lys Thr Leu Phe Ile Ser Arg Lys Thr Tyr
 865 870 875 880

Arg Ile Asp Gly Ser Gly Gln Met Ala Ile Thr Val Asp Val Glu Val
 885 890 895

Ala Ser Asp Thr Pro His Pro Ala Arg Ile Gly Leu Asn Cys Gln Leu
 900 905 910

Ala Gln Val Ala Glu Arg Val Asn Trp Leu Gly Leu Gly Pro Gln Glu
 915 920 925

Asn Tyr Pro Asp Arg Leu Thr Ala Ala Cys Phe Asp Arg Trp Asp Leu
 930 935 940

Pro Leu Ser Asp Met Tyr Thr Pro Tyr Val Phe Pro Ser Glu Asn Gly
 945 950 955 960

Leu Arg Cys Gly Thr Arg Glu Leu Asn Tyr Gly Pro His Gln Trp Arg
 965 970 975

Gly Asp Phe Gln Phe Asn Ile Ser Arg Tyr Ser Gln Gln Gln Leu Met
 980 985 990

Ser His Arg His Leu Leu His Ala Glu Glu Gly Thr Trp Leu Asn Ile
 995 1000 1005

Asp Gly Phe His Met Gly Ile Gly Gly Asp Asp Ser Trp Ser Pro
 1010 1015 1020

40

Ser Val Ser Ala Glu Leu Gln Leu Ser Ala Gly Arg Tyr His Tyr
 1025 1030 1035

Gln Leu Val Trp Cys Gln Lys
 1040 1045

<210> 25
 <211> 238
 <212> PRT
 <213> enhanced green fluorescence protein (eGFP)

<400> 25

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 26
 <211> 264
 <212> PRT
 <213> yellow fluorescent protein

<400> 26

Met Asp Gly Thr Glu Leu Gly Ser Thr Arg Asp Ser Arg Gly Ser Gly
 1 5 10 15

Gly Ser Gly Gly Ser Gly Gly Ser Gly Met Val Ser Lys Gly Glu Glu
 20 25 30

Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
 35 40 45

Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
 50 55 60

Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
 65 70 75 80

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
 85 90 95

Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
 100 105 110

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
 115 120 125

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
 130 135 140

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
 145 150 155 160

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
 165 170 175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
 180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
 195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
 210 215 220

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
 225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
 245 250 255

Leu Gly Met Asp Glu Leu Tyr Lys
 260

<210> 27
 <211> 238
 <212> PRT
 <213> soluble modified blue fluorescent protein

<400> 27

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 28

<211> 238

<212> PRT

<213> soluble-modified red-shifted green fluorescent protein

<400> 28

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Ser Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 29
 <211> 262
 <212> PRT
 <213> cyan fluorescent protein

<400> 29

Met His His His His His His His Asp Gly Thr Met Val Ser Lys Gly
 1 5 10 15

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
 20 25 30

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
 35 40 45

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
 50 55 60

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val
 65 70 75 80

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
 85 90 95

45

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
 100 105 110

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
 115 120 125

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
 130 135 140

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
 145 150 155 160

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
 165 170 175

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
 180 185 190

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
 195 200 205

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
 210 215 220

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
 225 230 235 240

Ile Thr Leu Gly Met Asp Glu Leu Tyr Ser Gly Ser Gly Ser Gly Ser
 245 250 255

Leu Glu Gly Thr Glu Leu
 260

<210> 30
 <211> 8
 <212> PRT
 <213> streptavidin binding sequence

<400> 30

Trp Ser His Pro Gln Phe Glu Lys
 1 5

<210> 31
 <211> 574
 <212> PRT
 <213> strepsolysin-O

<400> 31

Met Lys Asp Met Ser Asn Lys Lys Thr Phe Lys Lys Tyr Ser Arg Val
 1 5 10 15
 Ala Gly Leu Leu Thr Ala Ala Leu Ile Ile Gly Asn Leu Val Thr Ala
 20 25 30
 Asn Ala Glu Ser Asn Lys Gln Asn Thr Ala Ser Thr Glu Thr Thr Thr
 35 40 45
 Thr Asn Glu Gln Pro Lys Pro Glu Ser Ser Glu Leu Thr Thr Glu Lys
 50 55 60
 Ala Gly Gln Lys Thr Asp Asp Met Leu Asn Ser Asn Asp Met Ile Lys
 65 70 75 80
 Leu Ala Pro Lys Glu Met Pro Leu Glu Ser Ala Glu Lys Glu Glu Lys
 85 90 95
 Lys Ser Glu Asp Lys Lys Lys Ser Glu Glu Asp His Thr Glu Glu Ile
 100 105 110
 Asn Asp Lys Ile Tyr Ser Leu Asn Tyr Asn Glu Leu Glu Val Leu Ala
 115 120 125
 Lys Asn Gly Glu Thr Ile Glu Asn Phe Val Pro Lys Glu Gly Val Lys
 130 135 140
 Lys Ala Asp Lys Phe Ile Val Ile Glu Arg Lys Lys Lys Asn Ile Asn
 145 150 155 160
 Thr Thr Pro Val Asp Ile Ser Ile Ile Asp Ser Val Thr Asp Arg Thr
 165 170 175
 Tyr Pro Ala Ala Leu Gln Leu Ala Asn Lys Gly Phe Thr Glu Asn Lys
 180 185 190
 Pro Asp Ala Val Val Thr Lys Arg Asn Pro Gln Lys Ile His Ile Asp
 195 200 205
 Leu Pro Gly Met Gly Asp Lys Ala Thr Val Glu Val Asn Asp Pro Thr
 210 215 220
 Tyr Ala Asn Val Ser Thr Ala Ile Asp Asn Leu Val Asn Gln Trp His
 225 230 235 240
 Asp Asn Tyr Ser Gly Gly Asn Thr Leu Pro Ala Arg Thr Gln Tyr Thr
 245 250 255

Glu Ser Met Val Tyr Ser Lys Ser Gln Ile Glu Ala Ala Leu Asn Val
 260 265 270

Asn Ser Lys Ile Leu Asp Gly Thr Leu Gly Ile Asp Phe Lys Ser Ile
 275 280 285

Ser Lys Gly Glu Lys Lys Val Met Ile Ala Ala Tyr Lys Gln Ile Phe
 290 295 300

Tyr Thr Val Ser Ala Asn Leu Pro Asn Asn Pro Ala Asp Val Phe Asp
 305 310 315 320

Lys Ser Val Thr Phe Lys Glu Leu Gln Arg Lys Gly Val Ser Asn Glu
 325 330 335

Ala Pro Pro Leu Phe Val Ser Asn Val Ala Tyr Gly Arg Thr Val Phe
 340 345 350

Val Lys Leu Glu Thr Ser Ser Lys Ser Asn Asp Val Glu Ala Ala Phe
 355 360 365

Ser Ala Ala Leu Lys Gly Thr Asp Val Lys Thr Asn Gly Lys Tyr Ser
 370 375 380

Asp Ile Leu Glu Asn Ser Ser Phe Thr Ala Val Val Leu Gly Gly Asp
 385 390 395 400

Ala Ala Glu His Asn Lys Val Val Thr Lys Asp Phe Asp Val Ile Arg
 405 410 415

Asn Val Ile Lys Asp Asn Ala Thr Phe Ser Arg Lys Asn Pro Ala Tyr
 420 425 430

Pro Ile Ser Tyr Thr Ser Val Phe Leu Lys Asn Asn Lys Ile Ala Gly
 435 440 445

Val Asn Asn Arg Thr Glu Tyr Val Glu Thr Thr Ser Thr Glu Tyr Thr
 450 455 460

Ser Gly Lys Ile Asn Leu Ser His Arg Gly Ala Tyr Val Ala Gln Tyr
 465 470 475 480

Glu Ile Leu Trp Asp Glu Ile Asn Tyr Asp Asp Lys Gly Lys Glu Val
 485 490 495

Ile Thr Lys Arg Arg Trp Asp Asn Asn Trp Tyr Ser Lys Thr Ser Pro

48

500 505 510
 Phe Ser Thr Val Ile Pro Leu Gly Ala Asn Ser Arg Asn Ile Arg Ile
 515 520 525
 Met Ala Arg Glu Cys Thr Gly Leu Ala Trp Glu Trp Trp Arg Lys Val
 530 535 540
 Ile Asp Glu Arg Asp Val Lys Leu Ser Lys Glu Ile Asn Val Asn Ile
 545 550 555 560
 Ser Gly Ser Thr Leu Ser Pro Tyr Gly Ser Ile Thr Tyr Lys
 565 570
 <210> 32
 <211> 293
 <212> PRT
 <213> alpha-hemolysin
 <400> 32
 Ala Asp Ser Asp Ile Asn Ile Lys Thr Gly Thr Thr Asp Ile Gly Ser
 1 5 10 15
 Asn Thr Thr Val Lys Thr Gly Asp Leu Val Thr Tyr Asp Lys Glu Asn
 20 25 30
 Gly Met His Lys Lys Val Phe Tyr Ser Phe Ile Asp Asp Lys Asn His
 35 40 45
 Asn Lys Lys Leu Leu Val Ile Arg Thr Lys Gly Thr Ile Ala Gly Gln
 50 55 60
 Tyr Arg Val Tyr Ser Glu Glu Gly Ala Asn Lys Ser Gly Leu Ala Trp
 65 70 75 80
 Pro Ser Ala Phe Lys Val Gln Leu Gln Leu Pro Asp Asn Glu Val Ala
 85 90 95
 Gln Ile Ser Asp Tyr Tyr Pro Arg Asn Ser Ile Asp Thr Lys Glu Tyr
 100 105 110
 Met Ser Thr Leu Thr Tyr Gly Phe Asn Gly Asn Val Thr Gly Asp Asp
 115 120 125
 Thr Gly Lys Ile Gly Gly Leu Ile Gly Ala Asn Val Ser Ile Gly His
 130 135 140
 Thr Leu Lys Tyr Val Gln Pro Asp Phe Lys Thr Ile Leu Glu Ser Pro

49

145 150 155 160
 Thr Asp Lys Lys Val Gly Trp Lys Val Ile Phe Asn Asn Met Val Asn
 165 170 175
 Gln Asn Trp Gly Pro Tyr Asp Arg Asp Ser Trp Asn Pro Val Tyr Gly
 180 185 190
 Asn Gln Leu Phe Met Lys Thr Arg Asn Gly Ser Met Lys Ala Ala Asp
 195 200 205
 Asn Phe Leu Asp Pro Asn Lys Ala Ser Ser Leu Leu Ser Ser Gly Phe
 210 215 220
 Ser Pro Asp Phe Ala Thr Val Ile Thr Met Asp Arg Lys Ala Ser Lys
 225 230 235 240
 Gln Gln Thr Asn Ile Asp Val Ile Tyr Glu Arg Val Arg Asp Asp Tyr
 245 250 255
 Gln Leu His Trp Thr Ser Thr Asn Trp Lys Gly Thr Asn Thr Lys Asp
 260 265 270
 Lys Trp Thr Asp Arg Ser Ser Glu Arg Tyr Lys Ile Asp Trp Glu Lys
 275 280 285
 Glu Glu Met Thr Asn
 290

 <210> 33
 <211> 527
 <212> PRT
 <213> tetanolysin-O

 <400> 33
 Met Asn Lys Asn Val Leu Lys Phe Val Ser Arg Ser Leu Leu Ile Phe
 1 5 10 15
 Ser Met Thr Gly Leu Ile Ser Asn Tyr Asn Ser Ser Asn Val Leu Ala
 20 25 30
 Lys Gly Asn Val Glu Glu His Ser Leu Ile Asn Asn Gly Gln Val Val
 35 40 45
 Thr Ser Asn Thr Lys Cys Asn Leu Ala Lys Asp Asn Ser Ser Asp Ile
 50 55 60
 Asp Lys Asn Ile Tyr Gly Leu Ser Tyr Asp Pro Arg Lys Ile Leu Ser

50

65		70		75		80									
Tyr	Asn	Gly	Glu	Gln	Val	Glu	Asn	Phe	Val	Pro	Ala	Glu	Gly	Phe	Glu
			85						90					95	
Asn	Pro	Asp	Lys	Phe	Ile	Val	Val	Lys	Arg	Glu	Lys	Lys	Ser	Ile	Ser
			100					105					110		
Asp	Ser	Thr	Ala	Asp	Ile	Ser	Ile	Ile	Asp	Ser	Ile	Asn	Asp	Arg	Thr
		115					120					125			
Tyr	Pro	Gly	Ala	Ile	Gln	Leu	Ala	Asn	Arg	Asn	Leu	Met	Glu	Asn	Lys
	130					135					140				
Pro	Asp	Ile	Ile	Ser	Cys	Glu	Arg	Lys	Pro	Ile	Thr	Ile	Ser	Val	Asp
145					150					155					160
Leu	Pro	Gly	Met	Ala	Glu	Asp	Gly	Lys	Lys	Val	Val	Asn	Ser	Pro	Thr
			165					170						175	
Tyr	Ser	Ser	Val	Asn	Ser	Ala	Ile	Asn	Ser	Ile	Leu	Asp	Thr	Trp	Asn
			180					185					190		
Ser	Lys	Tyr	Ser	Ser	Lys	Tyr	Thr	Ile	Pro	Thr	Arg	Met	Ser	Tyr	Ser
		195					200					205			
Asp	Thr	Met	Val	Tyr	Ser	Gln	Ser	Gln	Leu	Ser	Ala	Ala	Val	Gly	Cys
	210					215					220				
Asn	Phe	Lys	Ala	Leu	Asn	Lys	Ala	Leu	Asn	Ile	Asp	Phe	Asp	Ser	Ile
225					230					235					240
Phe	Lys	Gly	Glu	Lys	Lys	Val	Met	Leu	Leu	Ala	Tyr	Lys	Gln	Ile	Phe
				245					250					255	
Tyr	Thr	Val	Ser	Val	Asp	Pro	Pro	Asn	Arg	Pro	Ser	Asp	Leu	Phe	Gly
			260					265					270		
Asp	Ser	Val	Thr	Phe	Asp	Glu	Leu	Ala	Leu	Lys	Gly	Ile	Asn	Asn	Asn
		275					280					285			
Asn	Pro	Pro	Ala	Tyr	Val	Ser	Asn	Val	Ala	Tyr	Gly	Arg	Thr	Ile	Tyr
	290					295					300				
Val	Lys	Leu	Glu	Thr	Thr	Ser	Lys	Ser	Ser	His	Val	Lys	Ala	Ala	Phe
305					310					315					320

aattggaagc aaatgacatc acagcaggtc agagaaaaag ggttgagcgg caggcaccca	60
gagtagtagg tctttggcat taggagcttg agcccagacg gccctagcag ggaccccagc	120
gcccagagaga cc atg cag agg tcg cct ctg gaa aag gcc agc gtt gtc tcc	171
Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser	
1 5 10	
aaa ctt ttt ttc agc tgg acc aga cca att ttg agg aaa gga tac aga	219
Lys Leu Phe Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg	
15 20 25	
cag cgc ctg gaa ttg tca gac ata tac caa atc cct tct gtt gat tct	267
Gln Arg Leu Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser	
30 35 40 45	
gct gac aat cta tct gaa aaa ttg gaa aga gaa tgg gat aga gag ctg	315
Ala Asp Asn Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu	
50 55 60	
gct tca aag aaa aat cct aaa ctc att aat gcc ctt cgg cga tgt ttt	363
Ala Ser Lys Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe	
65 70 75	
ttc tgg aga ttt atg ttc tat gga atc ttt tta tat tta ggg gaa gtc	411
Phe Trp Arg Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val	
80 85 90	
acc aaa gca gta cag cct ctc tta ctg gga aga atc ata gct tcc tat	459
Thr Lys Ala Val Gln Pro Leu Leu Gly Arg Ile Ile Ala Ser Tyr	
95 100 105	
gac ccg gat aac aag gag gaa cgc tct atc gcg att tat cta ggc ata	507
Asp Pro Asp Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile	
110 115 120 125	
ggc tta tgc ctt ctc ttt att gtg agg aca ctg ctc cta cac cca gcc	555
Gly Leu Cys Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala	
130 135 140	
att ttt ggc ctt cat cac att gga atg cag atg aga ata gct atg ttt	603
Ile Phe Gly Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe	
145 150 155	
agt ttg att tat aag aag act tta aag ctg tca agc cgt gtt cta gat	651
Ser Leu Ile Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp	
160 165 170	
aaa ata agt att gga caa ctt gtt agt ctc ctt tcc aac aac ctg aac	699
Lys Ile Ser Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn	
175 180 185	
aaa ttt gat gaa gga ctt gca ttg gca cat ttc gtg tgg atc gct cct	747
Lys Phe Asp Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro	
190 195 200 205	
ttg caa gtg gca ctc ctc atg ggg cta atc tgg gag ttg tta cag gcg	795
Leu Gln Val Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala	
210 215 220	
tct gcc ttc tgt gga ctt ggt ttc ctg ata gtc ctt gcc ctt ttt cag	843
Ser Ala Phe Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln	
225 230 235	

gct ggg cta ggg aga atg atg atg aag tac aga gat cag aga gct ggg Ala Gly Leu Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly 240 245 250	891
aag atc agt gaa aga ctt gtg att acc tca gaa atg att gaa aat atc Lys Ile Ser Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile 255 260 265	939
caa tct gtt aag gca tac tgc tgg gaa gaa gca atg gaa aaa atg att Gln Ser Val Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile 270 275 280 285	987
gaa aac tta aga caa aca gaa ctg aaa ctg act cgg aag gca gcc tat Glu Asn Leu Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr 290 295 300	1035
gtg aga tac ttc aat agc tca gcc ttc ttc ttc tca ggg ttc ttt gtg Val Arg Tyr Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val 305 310 315	1083
gtg ttt tta tct gtg ctt ccc tat gca cta atc aaa gga atc atc ctc Val Phe Leu Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu 320 325 330	1131
cgg aaa ata ttc acc acc atc tca ttc tgc att gtt ctg cgc atg gcg Arg Lys Ile Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala 335 340 345	1179
gtc act cgg caa ttt ccc tgg gct gta caa aca tgg tat gac tct ctt Val Thr Arg Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu 350 355 360 365	1227
gga gca ata aac aaa ata cag gat ttc tta caa aag caa gaa tat aag Gly Ala Ile Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys 370 375 380	1275
aca ttg gaa tat aac tta acg act aca gaa gta gtg atg gag aat gta Thr Leu Glu Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val 385 390 395	1323
aca gcc ttc tgg gag gag gga ttt ggg gaa tta ttt gag aaa gca aaa Thr Ala Phe Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys 400 405 410	1371
caa aac aat aac aat aga aaa act tct aat ggt gat gac agc ctc ttc Gln Asn Asn Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe 415 420 425	1419
ttc agt aat ttc tca ctt ctt ggt act cct gtc ctg aaa gat att aat Phe Ser Asn Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn 430 435 440 445	1467
ttc aag ata gaa aga gga cag ttg ttg gcg gtt gct gga tcc act gga Phe Lys Ile Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly 450 455 460	1515
gca ggc aag act tca ctt cta atg atg att atg gga gaa ctg gag cct Ala Gly Lys Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro 465 470 475	1563
tca gag ggt aaa att aag cac agt gga aga att tca ttc tgt tct cag Ser Glu Gly Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln	1611

480	485	490	
ttt tcc tgg att atg cct ggc acc att aaa gaa aat atc atc ttt ggt Phe Ser Trp Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly 495 500 505			1659
gtt tcc tat gat gaa tat aga tac aga agc gtc atc aaa gca tgc caa Val Ser Tyr Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln 510 515 520 525			1707
cta gaa gag gac atc tcc aag ttt gca gag aaa gac aat ata gtt ctt Leu Glu Glu Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu 530 535 540			1755
gga gaa ggt gga atc aca ctg agt gga ggt caa cga gca aga att tct Gly Glu Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser 545 550 555			1803
tta gca aga gca gta tac aaa gat gct gat ttg tat tta tta gac tct Leu Ala Arg Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser 560 565 570			1851
cct ttt gga tac cta gat gtt tta aca gaa aaa gaa ata ttt gaa agc Pro Phe Gly Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser 575 580 585			1899
tgt gtc tgt aaa ctg atg gct aac aaa act agg att ttg gtc act tct Cys Val Cys Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser 590 595 600 605			1947
aaa atg gaa cat tta aag aaa gct gac aaa ata tta att ttg aat gaa Lys Met Glu His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu 610 615 620			1995
ggt agc agc tat ttt tat ggg aca ttt tca gaa ctc caa aat cta cag Gly Ser Ser Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln 625 630 635			2043
cca gac ttt agc tca aaa ctc atg gga tgt gat tct ttc gac caa ttt Pro Asp Phe Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe 640 645 650			2091
agt gca gaa aga aga aat tca atc cta act gag acc tta cac cgt ttc Ser Ala Glu Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe 655 660 665			2139
tca tta gaa gga gat gct cct gtc tcc tgg aca gaa aca aaa aaa caa Ser Leu Glu Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln 670 675 680 685			2187
tct ttt aaa cag act gga gag ttt ggg gaa aaa agg aag aat tct att Ser Phe Lys Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile 690 695 700			2235
ctc aat cca atc aac tct ata cga aaa ttt tcc att gtg caa aag act Leu Asn Pro Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr 705 710 715			2283
ccc tta caa atg aat ggc atc gaa gag gat tct gat gag cct tta gag Pro Leu Gln Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu 720 725 730			2331
aga agg ctg tcc tta gta cca gat tct gag cag gga gag gcg ata ctg			2379

Arg	Arg	Leu	Ser	Leu	Val	Pro	Asp	Ser	Glu	Gln	Gly	Glu	Ala	Ile	Leu	
735						740					745					
cct	cgc	atc	agc	gtg	atc	agc	act	ggc	ccc	acg	ctt	cag	gca	cga	agg	2427
Pro	Arg	Ile	Ser	Val	Ile	Ser	Thr	Gly	Pro	Thr	Leu	Gln	Ala	Arg	Arg	
750					755					760					765	
agg	cag	tct	gtc	ctg	aac	ctg	atg	aca	cac	tca	gtt	aac	càa	ggc	cag	2475
Arg	Gln	Ser	Val	Leu	Asn	Leu	Met	Thr	His	Ser	Val	Asn	Gln	Gly	Gln	
				770					775					780		
aac	att	cac	cga	aag	aca	aca	gca	tcc	aca	cga	aaa	gtg	tca	ctg	gcc	2523
Asn	Ile	His	Arg	Lys	Thr	Thr	Ala	Ser	Thr	Arg	Lys	Val	Ser	Leu	Ala	
			785					790					795			
cct	cag	gca	aac	ttg	act	gaa	ctg	gat	ata	tat	tca	aga	agg	tta	tct	2571
Pro	Gln	Ala	Asn	Leu	Thr	Glu	Leu	Asp	Ile	Tyr	Ser	Arg	Arg	Leu	Ser	
		800					805					810				
caa	gaa	act	ggc	ttg	gaa	ata	agt	gaa	gaa	att	aac	gaa	gaa	gac	tta	2619
Gln	Glu	Thr	Gly	Leu	Glu	Ile	Ser	Glu	Glu	Ile	Asn	Glu	Glu	Asp	Leu	
	815					820					825					
aag	gag	tgc	ctt	ttt	gat	gat	atg	gag	agc	ata	cca	gca	gtg	act	aca	2667
Lys	Glu	Cys	Leu	Phe	Asp	Asp	Met	Glu	Ser	Ile	Pro	Ala	Val	Thr	Thr	
830					835				840						845	
tgg	aac	aca	tac	ctt	cga	tat	att	act	gtc	cac	aag	agc	tta	att	ttt	2715
Trp	Asn	Thr	Tyr	Leu	Arg	Tyr	Ile	Thr	Val	His	Lys	Ser	Leu	Ile	Phe	
				850					855					860		
gtg	cta	att	tgg	tgc	tta	gta	att	ttt	ctg	gca	gag	gtg	gct	gct	tct	2763
Val	Leu	Ile	Trp	Cys	Leu	Val	Ile	Phe	Leu	Ala	Glu	Val	Ala	Ala	Ser	
			865					870					875			
ttg	gtt	gtg	ctg	tgg	ctc	ctt	gga	aac	act	cct	ctt	caa	gac	aaa	ggg	2811
Leu	Val	Val	Leu	Trp	Leu	Leu	Gly	Asn	Thr	Pro	Leu	Gln	Asp	Lys	Gly	
			880				885					890				
aat	agt	act	cat	agt	aga	aat	aac	agc	tat	gca	gtg	att	atc	acc	agc	2859
Asn	Ser	Thr	His	Ser	Arg	Asn	Asn	Ser	Tyr	Ala	Val	Ile	Ile	Thr	Ser	
			895			900					905					
acc	agt	tcg	tat	tat	gtg	ttt	tac	att	tac	gtg	gga	gta	gcc	gac	act	2907
Thr	Ser	Ser	Tyr	Tyr	Val	Phe	Tyr	Ile	Tyr	Val	Gly	Val	Ala	Asp	Thr	
					915					920					925	
ttg	ctt	gct	atg	gga	ttc	ttc	aga	ggc	cta	cca	ctg	gtg	cat	act	cta	2955
Leu	Leu	Ala	Met	Gly	Phe	Phe	Arg	Gly	Leu	Pro	Leu	Val	His	Thr	Leu	
				930					935					940		
atc	aca	gtg	tcg	aaa	att	tta	cac	cac	aaa	atg	tta	cat	tct	gtt	ctt	3003
Ile	Thr	Val	Ser	Lys	Ile	Leu	His	His	Lys	Met	Leu	His	Ser	Val	Leu	
			945					950					955			
caa	gca	cct	atg	tca	acc	ctc	aac	acg	ttg	aaa	gca	ggc	ggg	att	ctt	3051
Gln	Ala	Pro	Met	Ser	Thr	Leu	Asn	Thr	Leu	Lys	Ala	Gly	Gly	Ile	Leu	
			960				965					970				
aat	aga	ttc	tcc	aaa	gat	ata	gca	att	ttg	gat	gac	ctt	ctg	cct	ctt	3099
Asn	Arg	Phe	Ser	Lys	Asp	Ile	Ala	Ile	Leu	Asp	Asp	Leu	Leu	Pro	Leu	
		975				980					985					

acc ata ttt gac ttc atc cag ttg tta tta att gtg att gga gct ata Thr Ile Phe Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile 990 995 1000 1005	3147
gca gtt gtc gca gtt tta caa ccc tac atc ttt gtt gca aca gtg Ala Val Val Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val 1010 1015 1020	3192
cca gtg ata gtg gct ttt att atg ttg aga gca tat ttc ctc caa Pro Val Ile Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln 1025 1030 1035	3237
acc tca cag caa ctc aaa caa ctg gaa tct gaa ggc agg agt cca Thr Ser Gln Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro 1040 1045 1050	3282
att ttc act cat ctt gtt aca agc tta aaa gga cta tgg aca ctt Ile Phe Thr His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu 1055 1060 1065	3327
cgt gcc ttc gga cgg cag cct tac ttt gaa act ctg ttc cac aaa Arg Ala Phe Gly Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys 1070 1075 1080	3372
gct ctg aat tta cat act gcc aac tgg ttc ttg tac ctg tca aca Ala Leu Asn Leu His Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr 1085 1090 1095	3417
ctg cgc tgg ttc caa atg aga ata gaa atg att ttt gtc atc ttc Leu Arg Trp Phe Gln Met Arg Ile Glu Met Ile Phe Val Ile Phe 1100 1105 1110	3462
ttc att gct gtt acc ttc att tcc att tta aca aca gga gaa gga Phe Ile Ala Val Thr Phe Ile Ser Ile Leu Thr Thr Gly Glu Gly 1115 1120 1125	3507
gaa gga aga gtt ggt att atc ctg act tta gcc atg aat atc atg Glu Gly Arg Val Gly Ile Ile Leu Thr Leu Ala Met Asn Ile Met 1130 1135 1140	3552
agt aca ttg cag tgg gct gta aac tcc agc ata gat gtg gat agc Ser Thr Leu Gln Trp Ala Val Asn Ser Ser Ile Asp Val Asp Ser 1145 1150 1155	3597
ttg atg cga tct gtg agc cga gtc ttt aag ttc att gac atg cca Leu Met Arg Ser Val Ser Arg Val Phe Lys Phe Ile Asp Met Pro 1160 1165 1170	3642
aca gaa ggt aaa cct acc aag tca acc aaa cca tac aag aat ggc Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn Gly 1175 1180 1185	3687
caa ctc tcg aaa gtt atg att att gag aat tca cac gtg aag aaa Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His Val Lys Lys 1190 1195 1200	3732
gat gac atc tgg ccc tca ggg ggc caa atg act gtc aaa gat ctc Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys Asp Leu 1205 1210 1215	3777
aca gca aaa tac aca gaa ggt gga aat gcc ata tta gag aac att Thr Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn Ile 1220 1225 1230	3822

tcc ttc tca ata agt cct ggc cag agg gtg ggc ctc ttg gga aga Ser Phe Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg 1235 1240 1245	3867
act gga tca ggg aag agt act ttg tta tca gct ttt ttg aga cta Thr Gly Ser Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu 1250 1255 1260	3912
ctg aac act gaa gga gaa atc cag atc gat ggt gtg tct tgg gat Leu Asn Thr Glu Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp 1265 1270 1275	3957
tca ata act ttg caa cag tgg agg aaa gcc ttt gga gtg ata cca Ser Ile Thr Leu Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro 1280 1285 1290	4002
cag aaa gta ttt att ttt tct gga aca ttt aga aaa aac ttg gat Gln Lys Val Phe Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp 1295 1300 1305	4047
ccc tat gaa cag tgg agt gat caa gaa ata tgg aaa gtt gca gat Pro Tyr Glu Gln Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp 1310 1315 1320	4092
gag gtt ggg ctc aga tct gtg ata gaa cag ttt cct ggg aag ctt Glu Val Gly Leu Arg Ser Val Ile Glu Gln Phe Pro Gly Lys Leu 1325 1330 1335	4137
gac ttt gtc ctt gtg gat ggg ggc tgt gtc cta agc cat ggc cac Asp Phe Val Leu Val Asp Gly Gly Cys Val Leu Ser His Gly His 1340 1345 1350	4182
aag cag ttg atg tgc ttg gct aga tct gtt ctc agt aag gcg aag Lys Gln Leu Met Cys Leu Ala Arg Ser Val Leu Ser Lys Ala Lys 1355 1360 1365	4227
atc ttg ctg ctt gat gaa ccc agt gct cat ttg gat cca gta aca Ile Leu Leu Leu Asp Glu Pro Ser Ala His Leu Asp Pro Val Thr 1370 1375 1380	4272
tac caa ata att aga aga act cta aaa caa gca ttt gct gat tgc Tyr Gln Ile Ile Arg Arg Thr Leu Lys Gln Ala Phe Ala Asp Cys 1385 1390 1395	4317
aca gta att ctc tgt gaa cac agg ata gaa gca atg ctg gaa tgc Thr Val Ile Leu Cys Glu His Arg Ile Glu Ala Met Leu Glu Cys 1400 1405 1410	4362
caa caa ttt ttg gtc ata gaa gag aac aaa gtg cgg cag tac gat Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr Asp 1415 1420 1425	4407
tcc atc cag aaa ctg ctg aac gag agg agc ctc ttc cgg caa gcc Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala 1430 1435 1440	4452
atc agc ccc tcc gac agg gtg aag ctc ttt ccc cac cgg aac tca Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser 1445 1450 1455	4497
agc aag tgc aag tct aag ccc cag att gct gct ctg aaa gag gag Ser Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu	4542

58

1460	1465	1470	
aca gaa gaa gag gtg	caa gat aca agg ctt	tag agagcagcat	4585
Thr Glu Glu Glu Val	Gln Asp Thr Arg Leu		
1475	1480		
aaatgttgac atgggacatt tgctcatgga attggagctc gtgggacagt cacctcatgg			4645
aattggagct cgtggaacag ttacctctgc ctcagaaaac aaggatgaat taagtttttt			4705
tttaaaaaag aaacatttgg taaggggaat tgaggacact gatatgggtc ttgataaatg			4765
gcttcctggc aatagtcaaa ttgtgtgaaa ggtacttcaa atccttgaag atttaccact			4825
tgtgttttgc aagccagatt ttcctgaaaa cccttgccat gtgctagtaa ttggaaaggc			4885
agctctaaat gtcaatcagc ctagttgatc agcttattgt ctagtgaaac tcgttaattt			4945
gtagtgttgg agaagaactg aaatcatact tcttaggggt atgattaagt aatgataact			5005
ggaaacttca gcggtttata taagcttgta ttcctttttc tctcctctcc ccatgatgtt			5065
tagaaacaca actatattgt ttgctaagca ttccaactat ctcatttcca agcaagtatt			5125
agaataccac aggaaccaca agactgcaca tcaaaatatg cccattcaa catctagtga			5185
gcagtcagga aagagaactt ccagatcctg gaaatcaggg ttagtattgt ccaggctctac			5245
caaaaatctc aatatttcag ataatacaca tacatccctt acctgggaaa gggctgttat			5305
aatctttcac aggggacagg atggttcctt tgatgaagaa gttgatatgc cttttccaa			5365
ctccagaaag tgacaagctc acagacctt gaactagagt ttagctggaa aagtatgtta			5425
gtgcaaattg tcacaggaca gcccttctt ccacagaagc tccaggtaga ggggtgtgtaa			5485
gtagataggc catgggcact gtgggtagac acacatgaag tccaagcatt tagatgtata			5545
ggttgatggg ggtatgtttt caggctagat gtatgtactt catgctgtct acactaagag			5605
agaatgagag acacactgaa gaagcaccaa tcatgaatta gttttatatg cttctgtttt			5665
ataattttgt gaagcaaaat ttttctcta ggaaatattt attttaataa tgtttcaaac			5725
atatattaca atgctgtatt ttaaaagaat gattatgaat tacatttgta taaaataatt			5785
tttatatttg aaatattgac tttttatggc actagtattt ttatgaaata ttatgttaaa			5845
actgggacag gggagaacct agggtgatat taaccagggg ccatgaatca ccttttggtc			5905
tggagggaag ccttggggct gatcgagttg ttgccacag ctgtatgatt ccagccaga			5965
cacagcctct tagatgcagt tctgaagaag atggtaccac cagtctgact gtttccatca			6025
agggtacact gccttctcaa ctccaaactg actcttaaga agactgcatt atatttatta			6085
ctgtaagaaa atatcacttg tcaataaaat ccatacattt gtgt			6129

<210> 35

<211> 1480

<212> PRT

<213> Cystic Fibrosis Transmembrane Conductance Regulator (CFTR)

<400> 35

```

Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe
1           5           10           15

Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg Gln Arg Leu
          20           25           30

Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser Ala Asp Asn
          35           40           45

Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu Ala Ser Lys
          50           55           60

Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg
65           70           75           80

Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala
          85           90           95

Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp
          100          105          110

Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys
          115          120          125

Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly
          130          135          140

Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile
145          150          155          160

Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser
          165          170          175

Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp
          180          185          190

Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val
          195          200          205

Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe
          210          215          220

Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu
225          230          235          240

```


Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly Val Ser Tyr
 500 505 510

Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu Glu Glu
 515 520 525

Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly
 530 535 540

Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg
 545 550 555 560

Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly
 565 570 575

Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys
 580 585 590

Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu
 595 600 605

His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu Gly Ser Ser
 610 615 620

Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe
 625 630 635 640

Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu
 645 650 655

Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu
 660 665 670

Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys
 675 680 685

Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro
 690 695 700

Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln
 705 710 715 720

Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg Arg Leu
 725 730 735

Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro Arg Ile
 740 745 750

Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg Gln Ser
 755 760 765

Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn Ile His
 770 775 780

Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro Gln Ala
 785 790 795 800

Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln Glu Thr
 805 810 815

Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys Glu Cys
 820 825 830

Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr Trp Asn Thr
 835 840 845

Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val Leu Ile
 850 855 860

Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu Val Val
 865 870 875 880

Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn Ser Thr
 885 890 895

His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser Thr Ser Ser
 900 905 910

Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr Leu Leu Ala
 915 920 925

Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile Thr Val
 930 935 940

Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln Ala Pro
 945 950 955 960

Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe
 965 970 975

Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe
 980 985 990

Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val

995					1000					1005				
Ala Val	Leu Gln	Pro Tyr	Ile	Phe Val	Ala Thr	Val	Pro Val	Ile						
1010			1015			1020								
Val Ala	Phe Ile	Met Leu	Arg	Ala Tyr	Phe Leu	Gln	Thr Ser	Gln						
1025			1030			1035								
Gln Leu	Lys Gln	Leu Glu	Ser	Glu Gly	Arg Ser	Pro	Ile Phe	Thr						
1040			1045			1050								
His Leu	Val Thr	Ser Leu	Lys	Gly Leu	Trp Thr	Leu	Arg Ala	Phe						
1055			1060			1065								
Gly Arg	Gln Pro	Tyr Phe	Glu	Thr Leu	Phe His	Lys	Ala Leu	Asn						
1070			1075			1080								
Leu His	Thr Ala	Asn Trp	Phe	Leu Tyr	Leu Ser	Thr	Leu Arg	Trp						
1085			1090			1095								
Phe Gln	Met Arg	Ile Glu	Met	Ile Phe	Val Ile	Phe	Phe Ile	Ala						
1100			1105			1110								
Val Thr	Phe Ile	Ser Ile	Leu	Thr Thr	Gly Glu	Gly	Glu Gly	Arg						
1115			1120			1125								
Val Gly	Ile Ile	Leu Thr	Leu	Ala Met	Asn Ile	Met	Ser Thr	Leu						
1130			1135			1140								
Gln Trp	Ala Val	Asn Ser	Ser	Ile Asp	Val Asp	Ser	Leu Met	Arg						
1145			1150			1155								
Ser Val	Ser Arg	Val Phe	Lys	Phe Ile	Asp Met	Pro	Thr Glu	Gly						
1160			1165			1170								
Lys Pro	Thr Lys	Ser Thr	Lys	Pro Tyr	Lys Asn	Gly	Gln Leu	Ser						
1175			1180			1185								
Lys Val	Met Ile	Ile Glu	Asn	Ser His	Val Lys	Lys	Asp Asp	Ile						
1190			1195			1200								
Trp Pro	Ser Gly	Gly Gln	Met	Thr Val	Lys Asp	Leu	Thr Ala	Lys						
1205			1210			1215								
Tyr Thr	Glu Gly	Gly Asn	Ala	Ile Leu	Glu Asn	Ile	Ser Phe	Ser						
1220			1225			1230								

Ile Ser 1235	Pro Gly Gln Arg 1240	Val Gly Leu Leu Gly Arg 1245	Thr Gly Ser
Gly Lys 1250	Ser Thr Leu Leu Ser 1255	Ala Phe Leu Arg Leu 1260	Leu Asn Thr
Glu Gly 1265	Glu Ile Gln Ile Asp 1270	Gly Val Ser Trp Asp 1275	Ser Ile Thr
Leu Gln 1280	Gln Trp Arg Lys 1285	Phe Gly Val Ile Pro 1290	Gln Lys Val
Phe Ile 1295	Phe Ser Gly Thr Phe 1300	Arg Lys Asn Leu Asp 1305	Pro Tyr Glu
Gln Trp 1310	Ser Asp Gln Glu Ile 1315	Trp Lys Val Ala Asp 1320	Glu Val Gly
Leu Arg 1325	Ser Val Ile Glu Gln 1330	Phe Pro Gly Lys Leu 1335	Asp Phe Val
Leu Val 1340	Asp Gly Gly Cys Val 1345	Leu Ser His Gly His 1350	Lys Gln Leu
Met Cys 1355	Leu Ala Arg Ser Val 1360	Leu Ser Lys Ala Lys 1365	Ile Leu Leu
Leu Asp 1370	Glu Pro Ser Ala His 1375	Leu Asp Pro Val Thr 1380	Tyr Gln Ile
Ile Arg 1385	Arg Thr Leu Lys Gln 1390	Ala Phe Ala Asp Cys 1395	Thr Val Ile
Leu Cys 1400	Glu His Arg Ile Glu 1405	Ala Met Leu Glu Cys 1410	Gln Gln Phe
Leu Val 1415	Ile Glu Glu Asn Lys 1420	Val Arg Gln Tyr Asp 1425	Ser Ile Gln
Lys Leu 1430	Leu Asn Glu Arg Ser 1435	Leu Phe Arg Gln Ala 1440	Ile Ser Pro
Ser Asp 1445	Arg Val Lys Leu Phe 1450	Pro His Arg Asn Ser 1455	Ser Lys Cys
Lys Ser 1460	Lys Pro Gln Ile Ala 1465	Ala Leu Lys Glu Glu 1470	Thr Glu Glu

Glu Val Gln Asp Thr Arg Leu
1475 1480

<210> 36
<211> 3168
<212> DNA
<213> GLUT2

<220>
<221> CDS
<222> (39)..(1613)
<223>

<400> 36
cacaagacct ggaattgaca ggactcccaa ctagtaca atg aca gaa gat aag gtc 56
Met Thr Glu Asp Lys Val
1 5

act ggg acc ctg gtt ttc act gtc atc act gct gtg ctg ggt tcc ttc 104
Thr Gly Thr Leu Val Phe Thr Val Ile Thr Ala Val Leu Gly Ser Phe
10 15 20

cag ttt gga tat gac att ggt gtg atc aat gca cct caa cag gta ata 152
Gln Phe Gly Tyr Asp Ile Gly Val Ile Asn Ala Pro Gln Gln Val Ile
25 30 35

ata tct cac tat aga cat gtt ttg ggt gtt cca ctg gat gac cga aaa 200
Ile Ser His Tyr Arg His Val Leu Gly Val Pro Leu Asp Asp Arg Lys
40 45 50

gct atc aac aac tat gtt atc aac agt aca gat gaa ctg ccc aca atc 248
Ala Ile Asn Asn Tyr Val Ile Asn Ser Thr Asp Glu Leu Pro Thr Ile
55 60 65 70

tca tac tca atg aac cca aaa cca acc cct tgg gct gag gaa gag act 296
Ser Tyr Ser Met Asn Pro Lys Pro Thr Pro Trp Ala Glu Glu Glu Thr
75 80 85

gtg gca gct gct caa cta atc acc atg ctc tgg tcc ctg tct gta tcc 344
Val Ala Ala Ala Gln Leu Ile Thr Met Leu Trp Ser Leu Ser Val Ser
90 95 100

agc ttt gca gtt ggt gga atg act gca tca ttc ttt ggt ggg tgg ctt 392
Ser Phe Ala Val Gly Gly Met Thr Ala Ser Phe Phe Gly Gly Trp Leu
105 110 115

ggg gac aca ctt gga aga atc aaa gcc atg tta gta gca aac att ctg 440
Gly Asp Thr Leu Gly Arg Ile Lys Ala Met Leu Val Ala Asn Ile Leu
120 125 130

tca tta gtt gga gct ctc ttg atg ggg ttt tca aaa ttg gga cca tct 488
Ser Leu Val Gly Ala Leu Leu Met Gly Phe Ser Lys Leu Gly Pro Ser
135 140 145 150

cat ata ctt ata att gct gga aga agc ata tca gga cta tat tgt ggg 536
His Ile Leu Ile Ile Ala Gly Arg Ser Ile Ser Gly Leu Tyr Cys Gly
155 160 165

cta att tca ggc ctg gtt cct atg tat atc ggt gaa att gct cca acc 584
Leu Ile Ser Gly Leu Val Pro Met Tyr Ile Gly Glu Ile Ala Pro Thr
170 175 180

gct ctc agg gga gca ctt ggc act ttt cat cag ctg gcc atc gtc acg Ala Leu Arg Gly Ala Leu Gly Thr Phe His Gln Leu Ala Ile Val Thr 185 190 195	632
ggc att ctt att agt cag att att ggt ctt gaa ttt atc ttg ggc aat Gly Ile Leu Ile Ser Gln Ile Ile Gly Leu Glu Phe Ile Leu Gly Asn 200 205 210	680
tat gat ctg tgg cac atc ctg ctt ggc ctg tct ggt gtg cga gcc atc Tyr Asp Leu Trp His Ile Leu Leu Gly Leu Ser Gly Val Arg Ala Ile 215 220 225 230	728
ctt cag tct ctg cta ctc ttt ttc tgt cca gaa agc ccc aga tac ctt Leu Gln Ser Leu Leu Leu Phe Phe Cys Pro Glu Ser Pro Arg Tyr Leu 235 240 245	776
tac atc aag tta gat gag gaa gtc aaa gca aaa caa agc ttg aaa aga Tyr Ile Lys Leu Asp Glu Glu Val Lys Ala Lys Gln Ser Leu Lys Arg 250 255 260	824
ctc aga gga tat gat gat gtc acc aaa gat att aat gaa atg aga aaa Leu Arg Gly Tyr Asp Asp Val Thr Lys Asp Ile Asn Glu Met Arg Lys 265 270 275	872
gaa aga gaa gaa gca tcg agt gag cag aaa gtc tct ata att cag ctc Glu Arg Glu Glu Ala Ser Ser Glu Gln Lys Val Ser Ile Ile Gln Leu 280 285 290	920
ttc acc aat tcc agc tac cga cag cct att cta gtg gca ctg atg ctg Phe Thr Asn Ser Ser Tyr Arg Gln Pro Ile Leu Val Ala Leu Met Leu 295 300 305 310	968
cat gtg gct cag caa ttt tcc gga atc aat ggc att ttt tac tac tca His Val Ala Gln Phe Ser Gly Ile Asn Gly Ile Phe Tyr Tyr Ser 315 320 325	1016
acc agc att ttt cag acg gct ggt atc agc aaa cct gtt tat gca acc Thr Ser Ile Phe Gln Thr Ala Gly Ile Ser Lys Pro Val Tyr Ala Thr 330 335 340	1064
att gga gtt ggc gct gta aac atg gtt ttc act gct gtc tct gta ttc Ile Gly Val Gly Ala Val Asn Met Val Phe Thr Ala Val Ser Val Phe 345 350 355	1112
ctt gtg gag aag gca ggg cga cgt tct ctc ttt cta att gga atg agt Leu Val Glu Lys Ala Gly Arg Arg Ser Leu Phe Leu Ile Gly Met Ser 360 365 370	1160
ggg atg ttt gtt tgt gcc atc ttc atg tca gtg gga ctt gtg ctg ctg Gly Met Phe Val Cys Ala Ile Phe Met Ser Val Gly Leu Val Leu Leu 375 380 385 390	1208
aat aag ttc tct tgg atg agt tat gtg agc atg ata gcc atc ttc ctc Asn Lys Phe Ser Trp Met Ser Tyr Val Ser Met Ile Ala Ile Phe Leu 395 400 405	1256
ttt gtc agc ttc ttt gaa att ggg cca ggc ccg atc ccc tgg ttc atg Phe Val Ser Phe Phe Glu Ile Gly Pro Gly Pro Ile Pro Trp Phe Met 410 415 420	1304
gtg gct gag ttt ttc agt caa gga cca cgt cct gct gct tta gca ata Val Ala Glu Phe Phe Ser Gln Gly Pro Arg Pro Ala Ala Leu Ala Ile	1352

425	430	435	
gct gca ttc agc aat tgg acc tgc aat ttc att gta gct ctg tgt ttc			1400
Ala Ala Phe Ser Asn Trp Thr Cys Asn Phe Ile Val Ala Leu Cys Phe			
440	445	450	
cag tac att gcg gac ttc tgt gga cct tat gtg ttt ttc ctc ttt gct			1448
Gln Tyr Ile Ala Asp Phe Cys Gly Pro Tyr Val Phe Phe Leu Phe Ala			
455	460	465	470
gga gtg ctc ctg gcc ttt acc ctg ttc aca ttt ttt aaa gtt cca gaa			1496
Gly Val Leu Leu Ala Phe Thr Leu Phe Thr Phe Phe Lys Val Pro Glu			
	475	480	485
acc aaa gga aag tct ttt gag gaa att gct gca gaa ttc caa aag aag			1544
Thr Lys Gly Lys Ser Phe Glu Glu Ile Ala Ala Glu Phe Gln Lys Lys			
	490	495	500
agt ggc tca gcc cac agg cca aaa gct gct gta gaa atg aaa ttc cta			1592
Ser Gly Ser Ala His Arg Pro Lys Ala Ala Val Glu Met Lys Phe Leu			
	505	510	515
gga gct aca gag act gtg taa aaaaaaacc ctgctttttg acatgaacag			1643
Gly Ala Thr Glu Thr Val			
520			
aaacaataag ggaaccgtct gtttttaaatt gatgattcct tgagcatttt atatccacat			1703
ctttaagtat tgtttttat tttatgtgctc tcatcagaaa tgtcatcaaa tattaccaaa			1763
aaagtatttt ttttaagttag agaatatatt tttgatggta agactgtaat taagtaaacc			1823
aaaaaggcta gtttattttg ttacactaaa gggcagggtg ttctaataatt ttttagctctg			1883
ttctttataa caaggttctt ctaaaattga agagatttca acatatcatt tttttaacac			1943
ataactagaa acctgaggat gcaacaaata tttatatatt tgaatatcat taaattggaa			2003
ttttcttacc catatatctt atgttaaagg agatatggct agtggcaata agttccatgt			2063
taaaatagac aactcttcca tttattgcac tcagcttttt tcttgagtac tagaatttgt			2123
attttgctta aaattttact tttgttctgt attttcatgt ggaatggatt atagagtata			2183
ctaaaaaatg tctatagaga aaaactttca tttttggtag gcttatcaaa atctttcagc			2243
actcagaaaa gaaaaccatt ttagttcctt tatttaatgg ccaaatggtt tttgcaagat			2303
ttaacactaa aaaggtttca cctgatcata tagcgtgggt tatcagttaa cattaacatc			2363
tattataaaa ccatgttgat tcccttctg tacaatcctt tgagttatag tttgctttgc			2423
tttttaattg aggacagcct ggttttcaca tacactcaaa caatcatgag tcagacattt			2483
ggtatattac ctcaaattcc taataagttt gatcaaactc aatgtaagaa aatttgaagt			2543
aaaggattga tcactttgtt aaaaatattt tctgaattat tatgtctcaa aataagttga			2603
aaaggtaggg tttgaggatt cctgagtgtg ggcttctgaa acttcataaa tgttcagctt			2663
cagactttta tcaaaatccc tatttaattt tcctggaaag actgattgtt ttatgggtgtg			2723
ttcctaacat aaaataatcg tctcctttga catttccttc tttgtcttag ctgtatacag			2783

attctagcca aactattcta tggccattac taacacgcat tgtacactat ctatctgcct 2843
 ttacctacat aggcaaattg gaaatacaca gatgattaaa cagacttttag cttacagtca 2903
 attttacaat tatggaaata tagttctgat gggccccaaa agcttagcag ggtgctaacg 2963
 tatctctagg ctgttttctc caccaactgg agcactgata aatccttctt atgtttgctt 3023
 taatgtgtat tgaagaaaag cactttttaa aaagtactct ttaagagtga aataattaaa 3083
 aaccactgaa catttgcttt gttttctaaa gttgttcaca tatatgtaat ttagcagtc 3143
 aaagaacaag aaattgtttc ttttc 3168

<210> 37
 <211> 524
 <212> PRT
 <213> GLUT2

<400> 37

Met Thr Glu Asp Lys Val Thr Gly Thr Leu Val Phe Thr Val Ile Thr
 1 5 10 15

Ala Val Leu Gly Ser Phe Gln Phe Gly Tyr Asp Ile Gly Val Ile Asn
 20 25 30

Ala Pro Gln Gln Val Ile Ile Ser His Tyr Arg His Val Leu Gly Val
 35 40 45

Pro Leu Asp Asp Arg Lys Ala Ile Asn Asn Tyr Val Ile Asn Ser Thr
 50 55 60

Asp Glu Leu Pro Thr Ile Ser Tyr Ser Met Asn Pro Lys Pro Thr Pro
 65 70 75 80

Trp Ala Glu Glu Glu Thr Val Ala Ala Ala Gln Leu Ile Thr Met Leu
 85 90 95

Trp Ser Leu Ser Val Ser Ser Phe Ala Val Gly Gly Met Thr Ala Ser
 100 105 110

Phe Phe Gly Gly Trp Leu Gly Asp Thr Leu Gly Arg Ile Lys Ala Met
 115 120 125

Leu Val Ala Asn Ile Leu Ser Leu Val Gly Ala Leu Leu Met Gly Phe
 130 135 140

Ser Lys Leu Gly Pro Ser His Ile Leu Ile Ile Ala Gly Arg Ser Ile
 145 150 155 160

Ser Gly Leu Tyr Cys Gly Leu Ile Ser Gly Leu Val Pro Met Tyr Ile
 165 170 175

Gly Glu Ile Ala Pro Thr Ala Leu Arg Gly Ala Leu Gly Thr Phe His
 180 185 190

Gln Leu Ala Ile Val Thr Gly Ile Leu Ile Ser Gln Ile Ile Gly Leu
 195 200 205

Glu Phe Ile Leu Gly Asn Tyr Asp Leu Trp His Ile Leu Leu Gly Leu
 210 215 220

Ser Gly Val Arg Ala Ile Leu Gln Ser Leu Leu Leu Phe Phe Cys Pro
 225 230 235 240

Glu Ser Pro Arg Tyr Leu Tyr Ile Lys Leu Asp Glu Glu Val Lys Ala
 245 250 255

Lys Gln Ser Leu Lys Arg Leu Arg Gly Tyr Asp Asp Val Thr Lys Asp
 260 265 270

Ile Asn Glu Met Arg Lys Glu Arg Glu Glu Ala Ser Ser Glu Gln Lys
 275 280 285

Val Ser Ile Ile Gln Leu Phe Thr Asn Ser Ser Tyr Arg Gln Pro Ile
 290 295 300

Leu Val Ala Leu Met Leu His Val Ala Gln Gln Phe Ser Gly Ile Asn
 305 310 315 320

Gly Ile Phe Tyr Tyr Ser Thr Ser Ile Phe Gln Thr Ala Gly Ile Ser
 325 330 335

Lys Pro Val Tyr Ala Thr Ile Gly Val Gly Ala Val Asn Met Val Phe
 340 345 350

Thr Ala Val Ser Val Phe Leu Val Glu Lys Ala Gly Arg Arg Ser Leu
 355 360 365

Phe Leu Ile Gly Met Ser Gly Met Phe Val Cys Ala Ile Phe Met Ser
 370 375 380

Val Gly Leu Val Leu Leu Asn Lys Phe Ser Trp Met Ser Tyr Val Ser
 385 390 395 400

Met Ile Ala Ile Phe Leu Phe Val Ser Phe Phe Glu Ile Gly Pro Gly
 405 410 415

Pro Ile Pro Trp Phe Met Val Ala Glu Phe Phe Ser Gln Gly Pro Arg
 420 425 430

Pro Ala Ala Leu Ala Ile Ala Ala Phe Ser Asn Trp Thr Cys Asn Phe
 435 440 445

Ile Val Ala Leu Cys Phe Gln Tyr Ile Ala Asp Phe Cys Gly Pro Tyr
 450 455 460

Val Phe Phe Leu Phe Ala Gly Val Leu Leu Ala Phe Thr Leu Phe Thr
 465 470 475 480

Phe Phe Lys Val Pro Glu Thr Lys Gly Lys Ser Phe Glu Glu Ile Ala
 485 490 495

Ala Glu Phe Gln Lys Lys Ser Gly Ser Ala His Arg Pro Lys Ala Ala
 500 505 510

Val Glu Met Lys Phe Leu Gly Ala Thr Glu Thr Val
 515 520

<210> 38
 <211> 3915
 <212> DNA
 <213> GLUT3

<220>
 <221> CDS
 <222> (243)..(1733)
 <223>

<400> 38
 gtgggggtggg gtggggctgg gggcttgtcg ccctttcagg ctccaccctt tgcggagatt 60
 ataaatagtc atgatcccag cgagacccag agatgcctgt aatggtgaga ctttggatcc 120
 ttcctgagga cgtggagaaa actttctgct gagaaggaca ttttgaaggt tttgttggct 180
 gaaaaagctg tttctggaat cacccttaga tctttcttga agacttgaat tagattacag 240
 cg atg ggg aca cag aag gtc acc cca gct ctg ata ttt gcc atc aca 287
 Met Gly Thr Gln Lys Val Thr Pro Ala Leu Ile Phe Ala Ile Thr
 1 5 10 15
 gtt gct aca atc ggc tct ttc caa ttt ggc tac aac act ggg gtc atc 335
 Val Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile
 20 25 30
 aat gct cct gag aag atc ata aag gaa ttt atc aat aaa act ttg acg 383
 Asn Ala Pro Glu Lys Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr
 35 40 45
 gac aag gga aat gcc cca ccc tct gag gtg ctg ctc acg tct ctc tgg 431
 Asp Lys Gly Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Ser Leu Trp
 50 55 60

tcc ttg tct gtg gcc ata ttt tcc gtc ggg ggt atg atc ggc tcc ttt Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe 65 70 75	479
tcc gtc gga ctc ttc gtc aac cgc ttt ggc agg cgc aat tca atg ctg Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu 80 85 90 95	527
att gtc aac ctg ttg gct gtc act ggt ggc tgc ttt atg gga ctg tgt Ile Val Asn Leu Leu Ala Val Thr Gly Gly Cys Phe Met Gly Leu Cys 100 105 110	575
aaa gta gct aag tcg gtt gaa atg ctg atc ctg ggt cgc ttg gtt att Lys Val Ala Lys Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile 115 120 125	623
ggc ctc ttc tgc gga ctc tgc aca ggt ttt gtg ccc atg tac att gga Gly Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly 130 135 140	671
gag atc tcg cct act gcc ctg cgg ggt gcc ttt ggc act ctc aac cag Glu Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln 145 150 155	719
ctg ggc atc gtt gtt gga att ctg gtg gcc cag atc ttt ggt ctg gaa Leu Gly Ile Val Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu 160 165 170 175	767
ttc atc ctt ggg tct gaa gag cta tgg ccg ctg cta ctg ggt ttt acc Phe Ile Leu Gly Ser Glu Glu Leu Trp Pro Leu Leu Leu Gly Phe Thr 180 185 190	815
atc ctt cct gct atc cta caa agt gca gcc ctt cca ttt tgc cct gaa Ile Leu Pro Ala Ile Leu Gln Ser Ala Ala Leu Pro Phe Cys Pro Glu 195 200 205	863
agt ccc aga ttt ttg ctc att aac aga aaa gaa gag gag aat gct aag Ser Pro Arg Phe Leu Leu Ile Asn Arg Lys Glu Glu Glu Asn Ala Lys 210 215 220	911
cag atc ctc cag cgg ttg tgg ggc acc cag gat gta tcc caa gac atc Gln Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile 225 230 235	959
cag gag atg aaa gat gag agt gca agg atg tca caa gaa aag caa gtc Gln Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val 240 245 250 255	1007
acc gtg cta gag ctc ttt aga gtg tcc agc tac cga cag ccc atc atc Thr Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile 260 265 270	1055
att tcc att gtg ctc cag ctc tct cag cag ctc tct ggg atc aat gct Ile Ser Ile Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala 275 280 285	1103
gtg ttc tat tac tca aca gga atc ttc aag gat gca ggt gtt caa gag Val Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Glu 290 295 300	1151
ccc atc tat gcc acc atc ggc gcg ggt gtg gtt aat act atc ttc act Pro Ile Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Ile Phe Thr	1199

305	310	315	
gta gtt tct cta ttt ctg gtg gaa agg gca gga aga agg act ctg cat			1247
Val Val Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His			
320	325	330	335
atg ata ggc ctt gga ggg atg gct ttt tgt tcc acg ctc atg act gtt			1295
Met Ile Gly Leu Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val			
	340	345	350
tct ttg tta tta aag gat aac tat aat ggg atg agc ttt gtc tgt att			1343
Ser Leu Leu Leu Lys Asp Asn Tyr Asn Gly Met Ser Phe Val Cys Ile			
	355	360	365
ggg gct atc ttg gtc ttt gta gcc ttc ttt gaa att gga cca ggc ccc			1391
Gly Ala Ile Leu Val Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro			
	370	375	380
att ccc tgg ttt att gtg gcc gaa ctc ttc agc cag ggc ccc cgc cca			1439
Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro			
	385	390	395
gct gcg atg gca gtg gcc ggc tgc tcc aac tgg acc tcc aac ttc cta			1487
Ala Ala Met Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu			
400	405	410	415
gtc gga ttg ctc ttc ccc tcc gct gct cac tat tta gga gcc tac gtt			1535
Val Gly Leu Leu Phe Pro Ser Ala Ala His Tyr Leu Gly Ala Tyr Val			
	420	425	430
ttt att atc ttc acc ggc ttc ctc att acc ttc ttg gct ttt acc ttc			1583
Phe Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe			
	435	440	445
ttc aaa gtc cct gag acc cgt ggc agg act ttt gag gat atc aca cg			1631
Phe Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg			
	450	455	460
gcc ttt gaa ggg cag gca cac ggt gca gat aga tct gga aag gac ggc			1679
Ala Phe Glu Gly Gln Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly			
	465	470	475
gtc atg gag atg aac agc atc gag cct gct aag gag acc acc acc aat			1727
Val Met Glu Met Asn Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn			
480	485	490	495
gtc taa gtcgtgcctc cttccacctc cctcccgcca tgggaaagcc acctctccct			1783
Val			
caacaaggga gagacctcat caggatgaac ccaggacgct tctgaatgct gctacttaat			1843
tccttttctca tcccacgcac tccatgagca cccaaggct gcggtttgtt ggatcttcaa			1903
tggtttttta aattttatctt cctggacatc ctcttctgct taggagagac cgagtgaacc			1963
taccttcatt tcaggaggga ttggccgctt ggcacatgac aactttgcca gcttttcctc			2023
ccttggttc tgatattgcc gcactagggg atataggaga ggaaaagtaa ggtgcagttc			2083
ccccaacctc agacttacca ggaagcagat acatatgagt gtggaagccg gaggggtgtt			2143
atgtaagagc accttcctca cttccatata gctctactgt gcaaattaac ttgagtttta			2203

```

tttattttat cctctggttt aattacataa tttttttttt tttactttaa gtttcaggat 2263
acatgtgccg aatgtgcagg tttgttacat aggtatatat atgccatgat ggaaatattt 2323
atttttttta gcgtaatttt gccaaataat aaaaacagaa ggaaattgag attagagggg 2383
ggtgttttaa gagaggttat agagtagaag atttgatgct ggagagggtta aggtgcaata 2443
agaatttagg gagaaatgtt gttcattatt ggagggtaaa tgatgtggtg cctgaggctc 2503
gtacgttacc tcttaacaat ttctgtcctt cagatggaaa ctctttaact tctcgtaaaa 2563
gtcatatacc tatataataa agctactgat ttcttgagg ctttttttct taagataata 2623
gtttacatgt agtagtactt gaaatctagg attattaact aatatgggca ttgtagtta 2683
tgatggttga tgggttctaa ttttggtagg agtccaggga agagaaagtg atttctagaa 2743
agcctgttcc cctcactgga tgaaataact cttctctgta gtagtctcat tacttttgaa 2803
gtaatccgc cactatctc gtgggagagc catccaaata agaaacctaa aataattggt 2863
tcttggtaga gattcattat ttttccactt tggtcttttag gagatttttag gtgttgattt 2923
tctgttgtat ttttaactcat acctttaag gaattcccca aagaatgttt atagcaact 2983
tggaatttgt aacctcagct ctgggagagg atttttttct gagcgattat tatctaaagt 3043
gtgttgttgc tttaggtcca cggcacgctt gcgtatgtct gttaccatgt cactgtggtc 3103
ctatgccgaa tgccctcagg ggacttgaat ctttccaata aaccagggtt agacagtatg 3163
agtcaatgtg cagtgtagcc cacacttgag aggatgaatg tatgtgcact gtcactttgc 3223
tctgggtgga agtacgttat tgttgactta ttttctctgt gtttgttcct acagcccctt 3283
tttcatatgt tgctcagtct ccctttccct tcttggtgct tacacatctc agacccttta 3343
gccaaaccct tgtcagtac agtattttgg ttcttagttc tctgtgttcc ctctgtcct 3403
ggagcctttg aataaaaatg cacgtagctg aggcgggatg cgggtggctca cgcctgtaat 3463
cccagcactt tgggaggcct aggcgggcgg tcagggttc gagaccagtc tggccaacat 3523
cgtgaaaccc tgtctctact aaaaatgcaa aaattagccg ggcgtggtgg cgggcgcctg 3583
taatcccagc tacttgggaa gctgaggcgg gagaatcatg tgaaccggg acgcaggggt 3643
tgcagtgagc ggagatcgca tcattgcact ctagcctggg ccacagggcg agactccgtc 3703
tcaaaaaaaa aaaaatgcac atagctatcg agtgtgcttt agcttgaaaa ggtgaccttg 3763
caacttcagt tcaactttct ggctcctcaa acagtaggtt ggcagtaagg cagggtccca 3823
tttctcactg agaagattgt gaatatttcc atatggattt tctattgtta ctctggttct 3883
ttgttttaaa ataaaaattc tgaatgtaca cg 3915

```

<210> 39
<211> 496
<212> PRT

<213> GLUT3

<400> 39

Met Gly Thr Gln Lys Val Thr Pro Ala Leu Ile Phe Ala Ile Thr Val
 1 5 10 15

Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile Asn
 20 25 30

Ala Pro Glu Lys Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr Asp
 35 40 45

Lys Gly Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Ser Leu Trp Ser
 50 55 60

Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe Ser
 65 70 75 80

Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu Ile
 85 90 95

Val Asn Leu Leu Ala Val Thr Gly Gly Cys Phe Met Gly Leu Cys Lys
 100 105 110

Val Ala Lys Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile Gly
 115 120 125

Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly Glu
 130 135 140

Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln Leu
 145 150 155 160

Gly Ile Val Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu Phe
 165 170 175

Ile Leu Gly Ser Glu Glu Leu Trp Pro Leu Leu Leu Gly Phe Thr Ile
 180 185 190

Leu Pro Ala Ile Leu Gln Ser Ala Ala Leu Pro Phe Cys Pro Glu Ser
 195 200 205

Pro Arg Phe Leu Leu Ile Asn Arg Lys Glu Glu Glu Asn Ala Lys Gln
 210 215 220

Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile Gln
 225 230 235 240

Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val Thr
 245 250 255
 Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile Ile
 260 265 270
 Ser Ile Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val
 275 280 285
 Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Glu Pro
 290 295 300
 Ile Tyr Ala Thr Ile Gly Ala Gly Val Val Asn Thr Ile Phe Thr Val
 305 310 315 320
 Val Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Met
 325 330 335
 Ile Gly Leu Gly Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val Ser
 340 345 350
 Leu Leu Leu Lys Asp Asn Tyr Asn Gly Met Ser Phe Val Cys Ile Gly
 355 360 365
 Ala Ile Leu Val Phe Val Ala Phe Phe Glu Ile Gly Pro Gly Pro Ile
 370 375 380
 Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala
 385 390 395 400
 Ala Met Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu Val
 405 410 415
 Gly Leu Leu Phe Pro Ser Ala Ala His Tyr Leu Gly Ala Tyr Val Phe
 420 425 430
 Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe Phe
 435 440 445
 Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg Ala
 450 455 460
 Phe Glu Gly Gln Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly Val
 465 470 475 480
 Met Glu Met Asn Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn Val
 485 490 495

<210> 40
 <211> 2218
 <212> DNA
 <213> GLUT5

<220>
 <221> CDS
 <222> (1)..(1581)
 <223>

<400> 40
 ctt ctc tct cca ttc agt gca cgc gtt act ttg gct aaa agg agg tga 48
 Leu Leu Ser Pro Phe Ser Ala Arg Val Thr Leu Ala Lys Arg Arg
 1 5 10 15
 gcg gca ctc tgc cct tcc aga gca agc atg gag caa cag gat cag agc 96
 Ala Ala Leu Cys Pro Ser Arg Ala Ser Met Glu Gln Gln Asp Gln Ser
 20 25 30
 atg aag gaa ggg agg ctg acg ctt gtg ctt gcc ctg gca acc ctg ata 144
 Met Lys Glu Gly Arg Leu Thr Leu Val Leu Ala Leu Ala Thr Leu Ile
 35 40 45
 gct gcc ttt ggg tca tcc ttc cag tat ggg tac aac gtg gct gct gtc 192
 Ala Ala Phe Gly Ser Ser Phe Gln Tyr Gly Tyr Asn Val Ala Ala Val
 50 55 60
 aac tcc cca gca ctg ctc atg caa caa ttt tac aat gag act tac tat 240
 Asn Ser Pro Ala Leu Leu Met Gln Gln Phe Tyr Asn Glu Thr Tyr Tyr
 65 70 75
 ggt agg acc ggt gaa ttc atg gaa gac ttc ccc ttg acg ttg ctg tgg 288
 Gly Arg Thr Gly Glu Phe Met Glu Asp Phe Pro Leu Thr Leu Leu Trp
 80 85 90 95
 tct gta acc gtg tcc atg ttt cca ttt gga ggg ttt atc gga tcc ctc 336
 Ser Val Thr Val Ser Met Phe Pro Phe Gly Gly Phe Ile Gly Ser Leu
 100 105 110
 ctg gtc ggc ccc ttg gtg aat aaa ttt ggc aga aaa ggg gcc ttg ctg 384
 Leu Val Gly Pro Leu Val Asn Lys Phe Gly Arg Lys Gly Ala Leu Leu
 115 120 125
 ttc aac aac ata ttt tct atc gtg cct gcg atc tta atg gga tgc agc 432
 Phe Asn Asn Ile Phe Ser Ile Val Pro Ala Ile Leu Met Gly Cys Ser
 130 135 140
 aga gtc gcc aca tca ttt gag ctt atc att att tcc aga ctt ttg gtg 480
 Arg Val Ala Thr Ser Phe Glu Leu Ile Ile Ile Ser Arg Leu Leu Val
 145 150 155
 gga ata tgt gca ggt gta tct tcc aac gtg gtc ccc atg tac tta ggg 528
 Gly Ile Cys Ala Gly Val Ser Ser Asn Val Val Pro Met Tyr Leu Gly
 160 165 170 175
 gag ctg gcc cct aaa aac ctg cgg ggg gct ctc ggg gtg gtg ccc cag 576
 Glu Leu Ala Pro Lys Asn Leu Arg Gly Ala Leu Gly Val Val Pro Gln
 180 185 190
 ctc ttc atc act gtt ggc atc ctt gtg gcc cag atc ttt ggt ctt cgg 624
 Leu Phe Ile Thr Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Arg

195	200	205	
aat ctc ctt gca aac gta gat ggc tgg ccg atc ctg ctg ggg ctg acc Asn Leu Leu Ala Asn Val Asp Gly Trp Pro Ile Leu Leu Gly Leu Thr 210 215 220			672
ggg gtc ccc gcg gcg ctg cag ctc ctt ctg ctg ccc ttc ttc ccc gag Gly Val Pro Ala Ala Leu Gln Leu Leu Leu Leu Pro Phe Phe Pro Glu 225 230 235			720
agc ccc agg tac ctg ctg att cag aag aaa gac gaa gcg gcc gcc aag Ser Pro Arg Tyr Leu Leu Ile Gln Lys Lys Asp Glu Ala Ala Ala Lys 240 245 250 255			768
aaa gcc cta cag acg ctg cgc ggc tgg gac tct gtg gac agg gag gtg Lys Ala Leu Gln Thr Leu Arg Gly Trp Asp Ser Val Asp Arg Glu Val 260 265 270			816
gcc gag atc cgg cag gag gat gag gca gag aag gcc gcg gcc ttc atc Ala Glu Ile Arg Gln Glu Asp Glu Ala Glu Lys Ala Ala Gly Phe Ile 275 280 285			864
tcc gtg ctg aag ctg ttc cgg atg cgc tcg ctg cgc tgg cag ctg ctg Ser Val Leu Lys Leu Phe Arg Met Arg Ser Leu Arg Trp Gln Leu Leu 290 295 300			912
tcc atc atc gtc ctc atg ggc ggc cag cag ctg tcg ggc gtc aac gct Ser Ile Ile Val Leu Met Gly Gly Gln Gln Leu Ser Gly Val Asn Ala 305 310 315			960
atc tac tac tac gcg gac cag atc tac ctg agc gcc gcc gtg ccg gag Ile Tyr Tyr Tyr Ala Asp Gln Ile Tyr Leu Ser Ala Gly Val Pro Glu 320 325 330 335			1008
gag cac gtg cag tac gtg acg gcc gcc acc ggg gcc gtg aac gtg gtc Glu His Val Gln Tyr Val Thr Ala Gly Thr Gly Ala Val Asn Val Val 340 345 350			1056
atg acc ttc tgc gcc gtg ttc gtg gtg gag ctc ctg ggt cgg agg ctg Met Thr Phe Cys Ala Val Phe Val Glu Leu Leu Gly Arg Arg Leu 355 360 365			1104
ctg ctg ctg ctg ggc ttc tcc atc tgc ctc ata gcc tgc tgc gtg ctc Leu Leu Leu Leu Gly Phe Ser Ile Cys Leu Ile Ala Cys Cys Val Leu 370 375 380			1152
act gca gct ctg gca ctg cag gac aca gtg tcc tgg atg cca tac atc Thr Ala Ala Leu Ala Leu Gln Asp Thr Val Ser Trp Met Pro Tyr Ile 385 390 395			1200
agc atc gtc tgt gtc atc tcc tac gtc ata gga cat gcc ctc ggg ccc Ser Ile Val Cys Val Ile Ser Tyr Val Ile Gly His Ala Leu Gly Pro 400 405 410 415			1248
agt ccc ata ccc gcg ctg ctc atc act gag atc ttc ctg cag tcc tct Ser Pro Ile Pro Ala Leu Leu Ile Thr Glu Ile Phe Leu Gln Ser Ser 420 425 430			1296
cgg cca tct gcc ttc atg gtg ggg ggc agt gtg cac tgg ctc tcc aac Arg Pro Ser Ala Phe Met Val Gly Gly Ser Val His Trp Leu Ser Asn 435 440 445			1344
ttc acc gtg ggc ttg atc ttc ccg ttc atc cag gag ggc ctc gcc ccg			1392

Phe Thr Val Gly Leu Ile Phe Pro Phe Ile Gln Glu Gly Leu Gly Pro
 450 455 460
 tac agc ttc att gtc ttc gcc gtg atc tgc ctc ctc acc acc atc tac 1440
 Tyr Ser Phe Ile Val Phe Ala Val Ile Cys Leu Leu Thr Thr Ile Tyr
 465 470 475
 atc ttc ttg att gtc ccg gag acc aag gcc aag acg ttc ata gag atc 1488
 Ile Phe Leu Ile Val Pro Glu Thr Lys Ala Lys Thr Phe Ile Glu Ile
 480 485 490 495
 aac cag att ttc acc aag atg aat aag gtg tct gaa gtg tac ccg gaa 1536
 Asn Gln Ile Phe Thr Lys Met Asn Lys Ser Glu Val Tyr Pro Glu
 500 505 510
 aag gag gaa ctg aaa gag ctt cca cct gtc act tcg gaa cag tga 1581
 Lys Glu Glu Lys Lys Glu Leu Pro Val Thr Ser Glu Gln
 515 520 525
 ctctggagag gaagccagtg gagctggtct gccaggggct tcccactttg gcttattttt 1641
 ctgacttcta gctgtctgtg aatatccaga aataaaacaa ctctgatgtg gaatgcagtc 1701
 ctcatctcca gcctccccac ccagtgga actgtgcaaa gggctgcctt gctgttcttg 1761
 aagctgggct gtctctctcc atgttggcct gtcaccagac ccgagtcaat taaacagctg 1821
 gtctccact ttgtgtgttc agccttcgtg tggtcctgg taacgtggct ccaccttgat 1881
 gggtaacact ttgtgtggct cctggtaaca taacaacaac agttactata gtggtgagat 1941
 ggaaggaatc aaattttgcc agagaaacta actcgtggc cccaacaggc cttccggggc 2001
 catgggcatt tgtttagagc caaattcatc ctcttaccag atccttttcc agaaatacct 2061
 gtctaggaag gtgtgatgtc agaaacaatg acatccagaa agctgaggaa caggttcctg 2121
 tggagacact gagtcagaat tcttcatcca aattattttg ttagtggaat atggaattgc 2181
 ttctgtgtag tcaataaaat gaacctgatc acttttc 2218

<210> 41
 <211> 15
 <212> PRT
 <213> GLUT5

<400> 41

Leu Leu Ser Pro Phe Ser Ala Arg Val Thr Leu Ala Lys Arg Arg
 1 5 10 15

<210> 42
 <211> 510
 <212> PRT
 <213> GLUT5

<400> 42

Ala Ala Leu Cys Pro Ser Arg Ala Ser Met Glu Gln Gln Asp Gln Ser
 1 5 10 15

79

Met Lys Glu Gly Arg Leu Thr Leu Val Leu Ala Leu Ala Thr Leu Ile
 20 25 30
 Ala Ala Phe Gly Ser Ser Phe Gln Tyr Gly Tyr Asn Val Ala Ala Val
 35 40 45
 Asn Ser Pro Ala Leu Leu Met Gln Gln Phe Tyr Asn Glu Thr Tyr Tyr
 50 55 60
 Gly Arg Thr Gly Glu Phe Met Glu Asp Phe Pro Leu Thr Leu Leu Trp
 65 70 75 80
 Ser Val Thr Val Ser Met Phe Pro Phe Gly Gly Phe Ile Gly Ser Leu
 85 90 95
 Leu Val Gly Pro Leu Val Asn Lys Phe Gly Arg Lys Gly Ala Leu Leu
 100 105 110
 Phe Asn Asn Ile Phe Ser Ile Val Pro Ala Ile Leu Met Gly Cys Ser
 115 120 125
 Arg Val Ala Thr Ser Phe Glu Leu Ile Ile Ile Ser Arg Leu Leu Val
 130 135 140
 Gly Ile Cys Ala Gly Val Ser Ser Asn Val Val Pro Met Tyr Leu Gly
 145 150 155 160
 Glu Leu Ala Pro Lys Asn Leu Arg Gly Ala Leu Gly Val Val Pro Gln
 165 170 175
 Leu Phe Ile Thr Val Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Arg
 180 185 190
 Asn Leu Leu Ala Asn Val Asp Gly Trp Pro Ile Leu Leu Gly Leu Thr
 195 200 205
 Gly Val Pro Ala Ala Leu Gln Leu Leu Leu Leu Pro Phe Phe Pro Glu
 210 215 220
 Ser Pro Arg Tyr Leu Leu Ile Gln Lys Lys Asp Glu Ala Ala Ala Lys
 225 230 235 240
 Lys Ala Leu Gln Thr Leu Arg Gly Trp Asp Ser Val Asp Arg Glu Val
 245 250 255
 Ala Glu Ile Arg Gln Glu Asp Glu Ala Glu Lys Ala Ala Gly Phe Ile
 260 265 270

80

Ser Val Leu Lys Leu Phe Arg Met Arg Ser Leu Arg Trp Gln Leu Leu
 275 280 285

Ser Ile Ile Val Leu Met Gly Gly Gln Gln Leu Ser Gly Val Asn Ala
 290 295 300

Ile Tyr Tyr Tyr Ala Asp Gln Ile Tyr Leu Ser Ala Gly Val Pro Glu
 305 310 315 320

Glu His Val Gln Tyr Val Thr Ala Gly Thr Gly Ala Val Asn Val Val
 325 330 335

Met Thr Phe Cys Ala Val Phe Val Val Glu Leu Leu Gly Arg Arg Leu
 340 345 350

Leu Leu Leu Leu Gly Phe Ser Ile Cys Leu Ile Ala Cys Cys Val Leu
 355 360 365

Thr Ala Ala Leu Ala Leu Gln Asp Thr Val Ser Trp Met Pro Tyr Ile
 370 375 380

Ser Ile Val Cys Val Ile Ser Tyr Val Ile Gly His Ala Leu Gly Pro
 385 390 395 400

Ser Pro Ile Pro Ala Leu Leu Ile Thr Glu Ile Phe Leu Gln Ser Ser
 405 410 415

Arg Pro Ser Ala Phe Met Val Gly Gly Ser Val His Trp Leu Ser Asn
 420 425 430

Phe Thr Val Gly Leu Ile Phe Pro Phe Ile Gln Glu Gly Leu Gly Pro
 435 440 445

Tyr Ser Phe Ile Val Phe Ala Val Ile Cys Leu Leu Thr Thr Ile Tyr
 450 455 460

Ile Phe Leu Ile Val Pro Glu Thr Lys Ala Lys Thr Phe Ile Glu Ile
 465 470 475 480

Asn Gln Ile Phe Thr Lys Met Asn Lys Val Ser Glu Val Tyr Pro Glu
 485 490 495

Lys Glu Glu Leu Lys Glu Leu Pro Pro Val Thr Ser Glu Gln
 500 505 510

<210> 43

<211> 1580
 <212> DNA
 <213> GLUT6

<220>
 <221> CDS
 <222> (47)..(1570)
 <223>

<400> 43

```

tgctccagtc tgagcgccct ccgctcgccc cgagagagac ccggcc atg cag gag      55
                                   Met Gln Glu
                                   1

ccg ctg ctg gga gcc gag ggc ccg gac tac gac acc ttc ccc gag aag      103
Pro Leu Leu Gly Ala Glu Gly Pro Asp Tyr Asp Thr Phe Pro Glu Lys
  5                               10                               15

ccg ccc ccg tcg cca ggg gac agg gcg cgg gtc ggg acc ctg cag aac      151
Pro Pro Pro Ser Pro Gly Asp Arg Ala Arg Val Gly Thr Leu Gln Asn
20                               25                               30                               35

aaa agg gtg ttc ctg gcc acc ttc gcc gca gtg ctc ggc aat ttc agc      199
Lys Arg Val Phe Leu Ala Thr Phe Ala Ala Val Leu Gly Asn Phe Ser
                               40                               45                               50

ttt ggg tat gcc ctg gtc tac aca tcc cct gtc atc cca gcc ctg gag      247
Phe Gly Tyr Ala Leu Val Tyr Thr Ser Pro Val Ile Pro Ala Leu Glu
                               55                               60                               65

cgc tcc ttg gat cct gac ctg cat ctg acc aaa tcc cag gca tcc tgg      295
Arg Ser Leu Asp Pro Asp Leu His Leu Thr Lys Ser Gln Ala Ser Trp
                               70                               75                               80

ttt ggg tcc gtg ttc acc ctg gga gca gcg gcc gga ggc ctg agt gcc      343
Phe Gly Ser Val Phe Thr Leu Gly Ala Ala Ala Gly Gly Leu Ser Ala
                               85                               90                               95

atg atc ctc aac gac ctc ctg ggc cgg aag ctg agc atc atg ttc tca      391
Met Ile Leu Asn Asp Leu Leu Gly Arg Lys Leu Ser Ile Met Phe Ser
100                               105                               110                               115

gct gtg ccg tcg gcg gcc ggc tat gcg ctc atg gcg ggt gcg cac ggc      439
Ala Val Pro Ser Ala Ala Gly Tyr Ala Leu Met Ala Gly Ala His Gly
                               120                               125                               130

ctc tgg atg ctg ctg ctc gga agg acg ctg acg ggc ttc gcc ggg ggg      487
Leu Trp Met Leu Leu Leu Gly Arg Thr Leu Thr Gly Phe Ala Gly Gly
                               135                               140                               145

ctc aca gct gcc tgc atc ccg gtg tac gtg tct gag att gct ccc cca      535
Leu Thr Ala Ala Cys Ile Pro Val Tyr Val Ser Glu Ile Ala Pro Pro
                               150                               155                               160

ggc gtt cgt ggg gct ctg ggg gcc aca ccc cag ctc atg gca gtg ttc      583
Gly Val Arg Gly Ala Leu Gly Ala Thr Pro Gln Leu Met Ala Val Phe
                               165                               170                               175

gga tcc ctg tcc ctc tac gcc ctt ggc ctc ctg ctg ccg tgg cgc tgg      631
Gly Ser Leu Ser Leu Tyr Ala Leu Gly Leu Leu Leu Pro Trp Arg Trp
180                               185                               190                               195

ctg gct gtg gcc ggg gag gcg cct gtg ctc atc atg atc ctg ctg ctc      679

```

Leu	Ala	Val	Ala	Gly	Glu	Ala	Pro	Val	Leu	Ile	Met	Ile	Leu	Leu	Leu	
				200					205					210		
agc	ttc	atg	ccc	aac	tcg	ccg	cgc	ttc	ctg	ctc	tct	cgg	ggc	agg	gac	727
Ser	Phe	Met	Pro	Asn	Ser	Pro	Arg	Phe	Leu	Leu	Ser	Arg	Gly	Arg	Asp	
			215					220					225			
gaa	gag	gcc	ctg	cgg	gcg	ctg	gcc	tgg	ctg	cgt	ggg	acg	gac	gtc	gat	775
Glu	Glu	Ala	Leu	Arg	Ala	Leu	Ala	Trp	Leu	Arg	Gly	Thr	Asp	Val	Asp	
		230					235					240				
gtc	cac	tgg	gag	ttc	gag	cag	atc	cag	gac	aac	gtc	cgg	aga	cag	agc	823
Val	His	Trp	Glu	Phe	Glu	Gln	Ile	Gln	Asp	Asn	Val	Arg	Arg	Gln	Ser	
	245					250					255					
agc	cga	gta	tcg	tgg	gct	gag	gca	cgg	gcc	cca	cac	gtg	tgc	cgg	ccc	871
Ser	Arg	Val	Ser	Trp	Ala	Glu	Ala	Arg	Ala	Pro	His	Val	Cys	Arg	Pro	
260					265					270					275	
atc	acc	gtg	gcc	ttg	ctg	atg	cgc	ctc	ctg	cag	cag	ctg	acg	ggc	atc	919
Ile	Thr	Val	Ala	Leu	Leu	Met	Arg	Leu	Leu	Gln	Gln	Leu	Thr	Gly	Ile	
			280					285						290		
acg	ccc	atc	ctg	gtc	tac	ctg	cag	tcc	atc	ttc	gac	agc	acc	gct	gtc	967
Thr	Pro	Ile	Leu	Val	Tyr	Leu	Gln	Ser	Ile	Phe	Asp	Ser	Thr	Ala	Val	
			295					300					305			
ctg	ctg	ccc	ccc	aag	gac	gac	gca	gcc	atc	gtt	ggg	gcc	gtg	cgg	ctc	1015
Leu	Leu	Pro	Pro	Lys	Asp	Asp	Ala	Ala	Ile	Val	Gly	Ala	Val	Arg	Leu	
		310					315					320				
ctg	tcc	gtg	ctg	atc	gcc	gcc	ctc	acc	atg	gac	ctc	gca	ggc	cgc	aag	1063
Leu	Ser	Val	Leu	Ile	Ala	Ala	Leu	Thr	Met	Asp	Leu	Ala	Gly	Arg	Lys	
	325					330					335					
gtg	ctg	ctc	ttc	gtc	tca	gcg	gcc	atc	atg	ttt	gct	gcc	aac	ctg	act	1111
Val	Leu	Leu	Phe	Val	Ser	Ala	Ala	Ile	Met	Phe	Ala	Ala	Asn	Leu	Thr	
340					345				350					355		
ctg	ggg	ctg	tac	atc	cac	ttt	ggc	ccc	agg	cct	ctg	agc	ccc	aac	agc	1159
Leu	Gly	Leu	Tyr	Ile	His	Phe	Gly	Pro	Arg	Pro	Leu	Ser	Pro	Asn	Ser	
			360					365					370			
act	gcg	ggc	ctg	gaa	agc	gag	tcc	tgg	ggg	gac	ttg	gcg	cag	ccc	ctg	1207
Thr	Ala	Gly	Leu	Glu	Ser	Glu	Ser	Trp	Gly	Asp	Leu	Ala	Gln	Pro	Leu	
			375					380					385			
gca	gca	ccc	gct	ggc	tac	ctc	acc	ctg	gtg	ccc	ctg	ctg	gcc	acc	atg	1255
Ala	Ala	Pro	Ala	Gly	Tyr	Leu	Thr	Leu	Val	Pro	Leu	Leu	Ala	Thr	Met	
		390					395					400				
ctc	ttc	atc	atg	ggc	tac	gcc	gtg	ggc	tgg	ggt	ccc	atc	acc	tgg	ctg	1303
Leu	Phe	Ile	Met	Gly	Tyr	Ala	Val	Gly	Trp	Gly	Pro	Ile	Thr	Trp	Leu	
	405					410					415					
ctc	atg	tct	gag	gtc	ctg	ccc	ctg	cgt	gcc	cgt	ggc	gtg	gcc	tca	ggg	1351
Leu	Met	Ser	Glu	Val	Leu	Pro	Leu	Arg	Ala	Arg	Gly	Val	Ala	Ser	Gly	
420					425				430					435		
ctc	tgc	gtg	ctg	gcc	agc	tgg	ctc	acc	gcc	ttc	gtc	ctc	acc	aag	tcc	1399
Leu	Cys	Val	Leu	Ala	Ser	Trp	Leu	Thr	Ala	Phe	Val	Leu	Thr	Lys	Ser	
			440					445						450		

ttc ctg cca gtg gtg agc acc ttc ggc ctc cag gtg cct ttc ttc ttc 1447
 Phe Leu Pro Val Val Ser Thr Phe Gly Leu Gln Val Pro Phe Phe Phe
 455 460 465

ttc gcg gcc atc tgc ttg gtg agc ctg gtg ttc aca ggc tgc tgt gtg 1495
 Phe Ala Ala Ile Cys Leu Val Ser Leu Val Phe Thr Gly Cys Cys Val
 470 475 480

ccc gag acc aag gga cgg tcc ctg gag cag atc gag tcc ttc ttc cgc 1543
 Pro Glu Thr Lys Gly Arg Ser Leu Glu Gln Ile Glu Ser Phe Phe Arg
 485 490 495

atg ggg aga agg tcc ttc ttg cgc tag gtcaaggtcc 1580
 Met Gly Arg Arg Ser Phe Leu Arg
 500 505

<210> 44
 <211> 507
 <212> PRT
 <213> GLUT6

<400> 44

Met Gln Glu Pro Leu Leu Gly Ala Glu Gly Pro Asp Tyr Asp Thr Phe
 1 5 10 15

Pro Glu Lys Pro Pro Pro Ser Pro Gly Asp Arg Ala Arg Val Gly Thr
 20 25 30

Leu Gln Asn Lys Arg Val Phe Leu Ala Thr Phe Ala Ala Val Leu Gly
 35 40 45

Asn Phe Ser Phe Gly Tyr Ala Leu Val Tyr Thr Ser Pro Val Ile Pro
 50 55 60

Ala Leu Glu Arg Ser Leu Asp Pro Asp Leu His Leu Thr Lys Ser Gln
 65 70 75 80

Ala Ser Trp Phe Gly Ser Val Phe Thr Leu Gly Ala Ala Ala Gly Gly
 85 90 95

Leu Ser Ala Met Ile Leu Asn Asp Leu Leu Gly Arg Lys Leu Ser Ile
 100 105 110

Met Phe Ser Ala Val Pro Ser Ala Ala Gly Tyr Ala Leu Met Ala Gly
 115 120 125

Ala His Gly Leu Trp Met Leu Leu Leu Gly Arg Thr Leu Thr Gly Phe
 130 135 140

Ala Gly Gly Leu Thr Ala Ala Cys Ile Pro Val Tyr Val Ser Glu Ile
 145 150 155 160

Ala Pro Pro Gly Val Arg Gly Ala Leu Gly Ala Thr Pro Gln Leu Met
 165 170 175

Ala Val Phe Gly Ser Leu Ser Leu Tyr Ala Leu Gly Leu Leu Leu Pro
 180 185 190

Trp Arg Trp Leu Ala Val Ala Gly Glu Ala Pro Val Leu Ile Met Ile
 195 200 205

Leu Leu Leu Ser Phe Met Pro Asn Ser Pro Arg Phe Leu Leu Ser Arg
 210 215 220

Gly Arg Asp Glu Glu Ala Leu Arg Ala Leu Ala Trp Leu Arg Gly Thr
 225 230 235 240

Asp Val Asp Val His Trp Glu Phe Glu Gln Ile Gln Asp Asn Val Arg
 245 250 255

Arg Gln Ser Ser Arg Val Ser Trp Ala Glu Ala Arg Ala Pro His Val
 260 265 270

Cys Arg Pro Ile Thr Val Ala Leu Leu Met Arg Leu Leu Gln Gln Leu
 275 280 285

Thr Gly Ile Thr Pro Ile Leu Val Tyr Leu Gln Ser Ile Phe Asp Ser
 290 295 300

Thr Ala Val Leu Leu Pro Pro Lys Asp Asp Ala Ala Ile Val Gly Ala
 305 310 315 320

Val Arg Leu Leu Ser Val Leu Ile Ala Ala Leu Thr Met Asp Leu Ala
 325 330 335

Gly Arg Lys Val Leu Leu Phe Val Ser Ala Ala Ile Met Phe Ala Ala
 340 345 350

Asn Leu Thr Leu Gly Leu Tyr Ile His Phe Gly Pro Arg Pro Leu Ser
 355 360 365

Pro Asn Ser Thr Ala Gly Leu Glu Ser Glu Ser Trp Gly Asp Leu Ala
 370 375 380

Gln Pro Leu Ala Ala Pro Ala Gly Tyr Leu Thr Leu Val Pro Leu Leu
 385 390 395 400

Ala Thr Met Leu Phe Ile Met Gly Tyr Ala Val Gly Trp Gly Pro Ile
 405 410 415

85

Thr Trp Leu Leu Met Ser Glu Val Leu Pro Leu Arg Ala Arg Gly Val
 420 425 430

Ala Ser Gly Leu Cys Val Leu Ala Ser Trp Leu Thr Ala Phe Val Leu
 435 440 445

Thr Lys Ser Phe Leu Pro Val Val Ser Thr Phe Gly Leu Gln Val Pro
 450 455 460

Phe Phe Phe Phe Ala Ala Ile Cys Leu Val Ser Leu Val Phe Thr Gly
 465 470 475 480

Cys Cys Val Pro Glu Thr Lys Gly Arg Ser Leu Glu Gln Ile Glu Ser
 485 490 495

Phe Phe Arg Met Gly Arg Arg Ser Phe Leu Arg
 500 505

<210> 45
 <211> 1575
 <212> DNA
 <213> GLUT7

<220> .
 <221> CDS
 <222> (1)..(1575)
 <223>

<400> 45
 atg gag aac aaa gag gcg gga acc cct cca ccc att cca tcc agg gag 48
 Met Glu Asn Lys Glu Ala Gly Thr Pro Pro Pro Ile Pro Ser Arg Glu
 1 5 10 15
 ggg cgg ctc cag ccg acg ctg ttg ctg gcg aca ctg agc gcg gcc ttt 96
 Gly Arg Leu Gln Pro Thr Leu Leu Leu Ala Thr Leu Ser Ala Ala Phe
 20 25 30
 ggc tca gcc ttc cag tac ggc tac aac ctc tct gtg gtc aac acg ccg 144
 Gly Ser Ala Phe Gln Tyr Gly Tyr Asn Leu Ser Val Val Asn Thr Pro
 35 40 45
 cac aag gtg ggc aca agc tgt gga tgg ggc aat gtt ttc cag gtc ttc 192
 His Lys Val Gly Thr Ser Cys Gly Trp Gly Asn Val Phe Gln Val Phe
 50 55 60
 aag tca ttt tac aac gaa acc tac ttt gag cga cac gca aca ttc atg 240
 Lys Ser Phe Tyr Asn Glu Thr Tyr Phe Glu Arg His Ala Thr Phe Met
 65 70 75 80
 gac ggg aag ctc atg ctg ctt cta tgg tct tgc acc gtc tcc atg ttt 288
 Asp Gly Lys Leu Met Leu Leu Leu Trp Ser Cys Thr Val Ser Met Phe
 85 90 95
 cct ctg ggc ggc ctg ttg ggg tca ttg ctc gtg ggc ctg ctg gtt gat 336
 Pro Leu Gly Gly Leu Leu Gly Ser Leu Leu Val Gly Leu Leu Val Asp

100	105	110	
agc tgc ggc aga aag ggg acc ctg ctg atc aac aac atc ttt gcc atc Ser Cys Gly Arg Lys Gly Thr Leu Ile Asn Asn Ile Phe Ala Ile 115 120 125			384
atc ccc gcc atc ctg atg gga gtc agc aaa gtg gcc aag gct ttt gag Ile Pro Ala Ile Leu Met Gly Val Ser Lys Val Ala Lys Ala Phe Glu 130 135 140			432
ctg atc gtc ttt tcc cga gtg gtg ctg gga gtc tgt gca ggc atc tcc Leu Ile Val Phe Ser Arg Val Val Leu Gly Val Cys Ala Gly Ile Ser 145 150 155 160			480
tac agc gcc ctt ccc atg tac ctg gga gaa ctg gcc ccc aag aac ctg Tyr Ser Ala Leu Pro Met Tyr Leu Gly Glu Leu Ala Pro Lys Asn Leu 165 170 175			528
aga ggc atg gtg gga aca atg acc gag gtt ttc gtc atc gtt gga gtc Arg Gly Met Val Gly Thr Met Thr Glu Val Phe Val Ile Val Gly Val 180 185 190			576
ttc cta gca cag atc ttc agc ctc cag gcc atc ttg ggc aac ccg gca Phe Leu Ala Gln Ile Phe Ser Leu Gln Ala Ile Leu Gly Asn Pro Ala 195 200 205			624
ggc tgg ccg gtg ctt ctg gcg ctc aca ggg gtg ccc gcc ctg ctg cag Gly Trp Pro Val Leu Leu Ala Leu Thr Gly Val Pro Ala Leu Leu Gln 210 215 220			672
ctg ctg acc ctg ccc ttc ttc ccc gaa agc ccc cgc tac tcc ctg att Leu Leu Thr Leu Pro Phe Phe Pro Glu Ser Pro Arg Tyr Ser Leu Ile 225 230 235 240			720
cag aaa gga gat gaa gcc aca gcg cga caa gct ctg agg agg ctg aga Gln Lys Gly Asp Glu Ala Thr Ala Arg Gln Ala Leu Arg Arg Leu Arg 245 250 255			768
ggc cac acg gac atg gag gcc gag ctg gag gac atg cgt gcg gag gcc Gly His Thr Asp Met Glu Ala Glu Leu Glu Asp Met Arg Ala Glu Ala 260 265 270			816
cgg gcc gag cgc gcc gag ggc cac ctg tct gtg ctg cac ctc tgt gcc Arg Ala Glu Arg Ala Glu Gly His Leu Ser Val Leu His Leu Cys Ala 275 280 285			864
ctg cgg tcc ctg cgc tgg cag ctc ctc tcc atc atc gtg ctc atg gcc Leu Arg Ser Leu Arg Trp Gln Leu Leu Ser Ile Ile Val Leu Met Ala 290 295 300			912
ggc cag cag ctg tcg ggc atc aat gcg atc aac tac tat gcg gac acc Gly Gln Gln Leu Ser Gly Ile Asn Ala Ile Asn Tyr Tyr Ala Asp Thr 305 310 315 320			960
atc tac aca tct gcg ggc gtg gag gcc gct cac tcc caa tat gta acg Ile Tyr Thr Ser Ala Gly Val Glu Ala Ala His Ser Gln Tyr Val Thr 325 330 335			1008
gtg ggc tct ggc gtc gtc aac ata gtg atg acc atc acc tcg gct gtc Val Gly Ser Gly Val Val Asn Ile Val Met Thr Ile Thr Ser Ala Val 340 345 350			1056
ctt gtg gag cgg ctg gga cgg cgg cac ctc ctg ctg gcc ggc tac ggc			1104

Leu Val Glu Arg Leu Gly Arg Arg His Leu Leu Leu Ala Gly Tyr Gly
 355 360 365
 atc tgc ggc tct gcc tgc ctg gtg ctg acg gtg gtg ctc cta ttc cag 1152
 Ile Cys Gly Ser Ala Cys Leu Val Leu Thr Val Val Leu Leu Phe Gln
 370 375 380
 aac agg gtc ccc gag ctg tcc tac ctc ggc atc atc tgt gtc ttt gcc 1200
 Asn Arg Val Pro Glu Leu Ser Tyr Leu Gly Ile Ile Cys Val Phe Ala
 385 390 395 400
 tac atc gcg gga cat tcc att ggg ccc agt cct gtc ccc tcg gtg gtg 1248
 Tyr Ile Ala Gly His Ser Ile Gly Pro Ser Pro Val Pro Ser Val Val
 405 410 415
 agg acc gag atc ttc ctg cag tcc tcc cgg cgg gca gct ttc atg gtg 1296
 Arg Thr Glu Ile Phe Leu Gln Ser Ser Arg Arg Ala Ala Phe Met Val
 420 425 430
 gac ggg gca gtg cac tgg ctc acc aac ttc atc ata ggc ttc ctg ttc 1344
 Asp Gly Ala Val His Trp Leu Thr Asn Phe Ile Ile Gly Phe Leu Phe
 435 440 445
 cca tcc atc cag gag gcc atc ggt gcc tac agt ttc atc atc ttt gcc 1392
 Pro Ser Ile Gln Glu Ala Ile Gly Ala Tyr Ser Phe Ile Ile Phe Ala
 450 455 460
 gga atc tgc ctc ctc act gcg att tac atc tac gtg gtt att ccg gag 1440
 Gly Ile Cys Leu Leu Thr Ala Ile Tyr Ile Tyr Val Val Ile Pro Glu
 465 470 475 480
 acc aag ggc aaa aca ttt gtg gag ata aac cgc att ttt gcc aag aga 1488
 Thr Lys Gly Lys Thr Phe Val Glu Ile Asn Arg Ile Phe Ala Lys Arg
 485 490 495
 aac agg gtg aag ctt cca gag gag aaa gaa gaa acc att gat gct ggg 1536
 Asn Arg Val Lys Leu Pro Glu Glu Lys Glu Glu Thr Ile Asp Ala Gly
 500 505 510
 cct ccc aca gcc tct cct gcc aag gaa act tcc ttt tag 1575
 Pro Pro Thr Ala Ser Pro Ala Lys Glu Thr Ser Phe
 515 520
 <210> 46
 <211> 524
 <212> PRT
 <213> GLUT7
 <400> 46
 Met Glu Asn Lys Glu Ala Gly Thr Pro Pro Pro Ile Pro Ser Arg Glu
 1 5 10 15
 Gly Arg Leu Gln Pro Thr Leu Leu Leu Ala Thr Leu Ser Ala Ala Phe
 20 25 30
 Gly Ser Ala Phe Gln Tyr Gly Tyr Asn Leu Ser Val Val Asn Thr Pro
 35 40 45

88

His Lys Val Gly Thr Ser Cys Gly Trp Gly Asn Val Phe Gln Val Phe
 50 55 60

Lys Ser Phe Tyr Asn Glu Thr Tyr Phe Glu Arg His Ala Thr Phe Met
 65 70 75 80

Asp Gly Lys Leu Met Leu Leu Leu Trp Ser Cys Thr Val Ser Met Phe
 85 90 95

Pro Leu Gly Gly Leu Leu Gly Ser Leu Leu Val Gly Leu Leu Val Asp
 100 105 110

Ser Cys Gly Arg Lys Gly Thr Leu Leu Ile Asn Asn Ile Phe Ala Ile
 115 120 125

Ile Pro Ala Ile Leu Met Gly Val Ser Lys Val Ala Lys Ala Phe Glu
 130 135 140

Leu Ile Val Phe Ser Arg Val Val Leu Gly Val Cys Ala Gly Ile Ser
 145 150 155 160

Tyr Ser Ala Leu Pro Met Tyr Leu Gly Glu Leu Ala Pro Lys Asn Leu
 165 170 175

Arg Gly Met Val Gly Thr Met Thr Glu Val Phe Val Ile Val Gly Val
 180 185 190

Phe Leu Ala Gln Ile Phe Ser Leu Gln Ala Ile Leu Gly Asn Pro Ala
 195 200 205

Gly Trp Pro Val Leu Leu Ala Leu Thr Gly Val Pro Ala Leu Leu Gln
 210 215 220

Leu Leu Thr Leu Pro Phe Phe Pro Glu Ser Pro Arg Tyr Ser Leu Ile
 225 230 235 240

Gln Lys Gly Asp Glu Ala Thr Ala Arg Gln Ala Leu Arg Arg Leu Arg
 245 250 255

Gly His Thr Asp Met Glu Ala Glu Leu Glu Asp Met Arg Ala Glu Ala
 260 265 270

Arg Ala Glu Arg Ala Glu Gly His Leu Ser Val Leu His Leu Cys Ala
 275 280 285

Leu Arg Ser Leu Arg Trp Gln Leu Leu Ser Ile Ile Val Leu Met Ala
 290 295 300

89

Gly Gln Gln Leu Ser Gly Ile Asn Ala Ile Asn Tyr Tyr Ala Asp Thr
 305 310 315 320

Ile Tyr Thr Ser Ala Gly Val Glu Ala Ala His Ser Gln Tyr Val Thr
 325 330 335

Val Gly Ser Gly Val Val Asn Ile Val Met Thr Ile Thr Ser Ala Val
 340 345 350

Leu Val Glu Arg Leu Gly Arg Arg His Leu Leu Leu Ala Gly Tyr Gly
 355 360 365

Ile Cys Gly Ser Ala Cys Leu Val Leu Thr Val Val Leu Leu Phe Gln
 370 375 380

Asn Arg Val Pro Glu Leu Ser Tyr Leu Gly Ile Ile Cys Val Phe Ala
 385 390 395 400

Tyr Ile Ala Gly His Ser Ile Gly Pro Ser Pro Val Pro Ser Val Val
 405 410 415

Arg Thr Glu Ile Phe Leu Gln Ser Ser Arg Arg Ala Ala Phe Met Val
 420 425 430

Asp Gly Ala Val His Trp Leu Thr Asn Phe Ile Ile Gly Phe Leu Phe
 435 440 445

Pro Ser Ile Gln Glu Ala Ile Gly Ala Tyr Ser Phe Ile Ile Phe Ala
 450 455 460

Gly Ile Cys Leu Leu Thr Ala Ile Tyr Ile Tyr Val Val Ile Pro Glu
 465 470 475 480

Thr Lys Gly Lys Thr Phe Val Glu Ile Asn Arg Ile Phe Ala Lys Arg
 485 490 495

Asn Arg Val Lys Leu Pro Glu Glu Lys Glu Glu Thr Ile Asp Ala Gly
 500 505 510

Pro Pro Thr Ala Ser Pro Ala Lys Glu Thr Ser Phe
 515 520

<210> 47
 <211> 1508
 <212> DNA
 <213> GLUT8

<220>

<221> CDS

<222> (27)..(1460)

<223>

<400> 47

```

agctggccga tgcgttggcc gccgac atg acg ccc gag gac cca gag gaa acc      53
                        Met Thr Pro Glu Asp Pro Glu Glu Thr
                        1                      5

cag ccg ctt ctg ggg cct cct ggc ggc agc gcg ccc cgc ggc cgc cgc      101
Gln Pro Leu Leu Gly Pro Pro Gly Gly Ser Ala Pro Arg Gly Arg Arg
10                      15                      20                      25

gtc ttc ctc gcc gcc ttc gcc gct gcc ctg ggc cca ctc agc ttc ggc      149
Val Phe Leu Ala Ala Phe Ala Ala Ala Leu Gly Pro Leu Ser Phe Gly
                      30                      35                      40

ttc gcg ctc ggc tac agc tcc ccg gcc atc cct agc ctg cag cgc gcc      197
Phe Ala Leu Gly Tyr Ser Ser Pro Ala Ile Pro Ser Leu Gln Arg Ala
                      45                      50                      55

gcg ccc ccg gcc ccg cgc ctg gac gac gcc gcc gcc tcc tgg ttc ggg      245
Ala Pro Pro Ala Pro Arg Leu Asp Asp Ala Ala Ala Ser Trp Phe Gly
                      60                      65                      70

gct gtc gtg acc ctg ggt gcc gcg gcg ggg gga gtg ctg ggc ggc tgg      293
Ala Val Val Thr Leu Gly Ala Ala Ala Gly Gly Val Leu Gly Gly Trp
                      75                      80                      85

ctg gtg gac cgc gcc ggg cgc aag ctg agc ctc ttg ctg tgc tcc gtg      341
Leu Val Asp Arg Ala Gly Arg Lys Leu Ser Leu Leu Leu Cys Ser Val
90                      95                      100                      105

ccc ttc gtg gcc ggc ttt gcc gtc atc acc gcg gcc cag gac gtg tgg      389
Pro Phe Val Ala Gly Phe Ala Val Ile Thr Ala Ala Gln Asp Val Trp
                      110                      115                      120

atg ctg ctg ggg ggc cgc ctc ctc acc ggc ctg gcc tgc ggt gtt gcc      437
Met Leu Leu Gly Gly Arg Leu Leu Thr Gly Leu Ala Cys Gly Val Ala
                      125                      130                      135

tcc cta gtg gcc ccg gtc tac atc tcc gaa atc gcc tac cca gca gtc      485
Ser Leu Val Ala Pro Val Tyr Ile Ser Glu Ile Ala Tyr Pro Ala Val
                      140                      145                      150

cgg ggg ttg ctc ggc tcc tgt gtg cag cta atg gtc gtc gtc ggc atc      533
Arg Gly Leu Leu Gly Ser Cys Val Gln Leu Met Val Val Val Gly Ile
                      155                      160                      165

ctc ctg gcc tac ctg gca ggc tgg gtg ctg gag tgg cgc tgg ctg gct      581
Leu Leu Ala Tyr Leu Ala Gly Trp Val Leu Glu Trp Arg Trp Leu Ala
170                      175                      180                      185

gtg ctg ggc tgc gtg ccc ccc tcc ctc atg ctg ctt ctc atg tgc ttc      629
Val Leu Gly Cys Val Pro Pro Ser Leu Met Leu Leu Leu Met Cys Phe
                      190                      195                      200

atg ccc gag acc ccg cgc ttc ctg ctg act cag cac agg cgc cag gag      677
Met Pro Glu Thr Pro Arg Phe Leu Leu Thr Gln His Arg Arg Gln Glu
                      205                      210                      215

gcc atg gcc gcc ctg cgg ttc ctg tgg ggc tcc gag cag ggc tgg gaa      725
Ala Met Ala Ala Leu Arg Phe Leu Trp Gly Ser Glu Gln Gly Trp Glu

```

220	225	230	
gac ccc ccc atc ggg gct gag cag agc ttt cac ctg gcc ctg ctg cgg Asp Pro Pro Ile Gly Ala Glu Gln Ser Phe His Leu Ala Leu Leu Arg 235 240 245			773
cag ccc ggc atc tac aag ccc ttc atc atc ggc gtc tcc ctg atg gcc Gln Pro Gly Ile Tyr Lys Pro Phe Ile Ile Gly Val Ser Leu Met Ala 250 255 260 265			821
ttc cag cag ctg tcg ggg gtc aac gcc gtc atg ttc tat gca gag acc Phe Gln Gln Leu Ser Gly Val Asn Ala Val Met Phe Tyr Ala Glu Thr 270 275 280			869
atc ttt gaa gag gcc aag ttc aag gac agc agc ctg gcc tcg gtc gtc Ile Phe Glu Glu Ala Lys Phe Lys Asp Ser Ser Leu Ala Ser Val Val 285 290 295			917
gtg ggt gtc atc cag gtg ctg ttc aca gct gtg gcg gct ctc atc atg Val Gly Val Ile Gln Val Leu Phe Thr Ala Val Ala Ala Leu Ile Met 300 305 310			965
gac aga gca ggg cgg agg ctg ctc ctg gtc ttg tca ggt gtg gtc atg Asp Arg Ala Gly Arg Arg Leu Leu Leu Val Leu Ser Gly Val Val Met 315 320 325			1013
gtg ttc agc acg agt gcc ttc ggc gcc tac ttc aag ctg acc cag ggt Val Phe Ser Thr Ser Ala Phe Gly Ala Tyr Phe Lys Leu Thr Gln Gly 330 335 340 345			1061
ggc cct ggc aac tcc tcg cac gtg gcc atc tcg gcg cct gtc tct gca Gly Pro Gly Asn Ser Ser His Val Ala Ile Ser Ala Pro Val Ser Ala 350 355 360			1109
cag cct gtt gat gcc agc gtg ggg ctg gcc tgg ctg gcc gtg ggc agc Gln Pro Val Asp Ala Ser Val Gly Leu Ala Trp Leu Ala Val Gly Ser 365 370 375			1157
atg tgc ctc ttc atc gcc ggc ttt gcg gtg ggc tgg ggg ccc atc ccc Met Cys Leu Phe Ile Ala Gly Phe Ala Val Gly Trp Gly Pro Ile Pro 380 385 390			1205
tgg ctc ctc atg tca gag atc ttc cct ctg cat gtc aag ggc gtg gcg Trp Leu Leu Met Ser Glu Ile Phe Pro Leu His Val Lys Gly Val Ala 395 400 405			1253
aca ggc atc tgc gtc ctc acc aac tgg ctc atg gcc ttt ctc gtg acc Thr Gly Ile Cys Val Leu Thr Asn Trp Leu Met Ala Phe Leu Val Thr 410 415 420 425			1301
aag gag ttc agc agc ctc atg gag gtc ctc agg ccc tat gga gcc ttc Lys Glu Phe Ser Ser Leu Met Glu Val Leu Arg Pro Tyr Gly Ala Phe 430 435 440			1349
tgg ctt gcc tcc gct ttc tgc atc ttc agt gtc ctt ttc act ttt tcc Trp Leu Ala Ser Ala Phe Cys Ile Phe Ser Val Leu Phe Thr Phe Ser 445 450 455			1397
tgt gtc cct gaa act aaa gga aag act ctg gaa caa atc aca gcc cat Cys Val Pro Glu Thr Lys Gly Lys Thr Leu Glu Gln Ile Thr Ala His 460 465 470			1445
ttt gag ggg cga tga cagccactca ctaggggatg gagcaagcct gtgactccaa			1500

92

Phe Glu Gly Arg
475

gctgggcc

1508

<210> 48
<211> 477
<212> PRT
<213> GLUT8

<400> 48

Met Thr Pro Glu Asp Pro Glu Glu Thr Gln Pro Leu Leu Gly Pro Pro
1 5 10 15

Gly Gly Ser Ala Pro Arg Gly Arg Arg Val Phe Leu Ala Ala Phe Ala
20 25 30

Ala Ala Leu Gly Pro Leu Ser Phe Gly Phe Ala Leu Gly Tyr Ser Ser
35 40 45

Pro Ala Ile Pro Ser Leu Gln Arg Ala Ala Pro Pro Ala Pro Arg Leu
50 55 60

Asp Asp Ala Ala Ala Ser Trp Phe Gly Ala Val Val Thr Leu Gly Ala
65 70 75 80

Ala Ala Gly Gly Val Leu Gly Gly Trp Leu Val Asp Arg Ala Gly Arg
85 90 95

Lys Leu Ser Leu Leu Leu Cys Ser Val Pro Phe Val Ala Gly Phe Ala
100 105 110

Val Ile Thr Ala Ala Gln Asp Val Trp Met Leu Leu Gly Gly Arg Leu
115 120 125

Leu Thr Gly Leu Ala Cys Gly Val Ala Ser Leu Val Ala Pro Val Tyr
130 135 140

Ile Ser Glu Ile Ala Tyr Pro Ala Val Arg Gly Leu Leu Gly Ser Cys
145 150 155 160

Val Gln Leu Met Val Val Val Gly Ile Leu Leu Ala Tyr Leu Ala Gly
165 170 175

Trp Val Leu Glu Trp Arg Trp Leu Ala Val Leu Gly Cys Val Pro Pro
180 185 190

Ser Leu Met Leu Leu Leu Met Cys Phe Met Pro Glu Thr Pro Arg Phe
195 200 205

Leu Leu Thr Gln His Arg Arg Gln Glu Ala Met Ala Ala Leu Arg Phe
 210 215 220

Leu Trp Gly Ser Glu Gln Gly Trp Glu Asp Pro Pro Ile Gly Ala Glu
 225 230 235 240

Gln Ser Phe His Leu Ala Leu Leu Arg Gln Pro Gly Ile Tyr Lys Pro
 245 250 255

Phe Ile Ile Gly Val Ser Leu Met Ala Phe Gln Gln Leu Ser Gly Val
 260 265 270

Asn Ala Val Met Phe Tyr Ala Glu Thr Ile Phe Glu Glu Ala Lys Phe
 275 280 285

Lys Asp Ser Ser Leu Ala Ser Val Val Val Gly Val Ile Gln Val Leu
 290 295 300

Phe Thr Ala Val Ala Ala Leu Ile Met Asp Arg Ala Gly Arg Arg Leu
 305 310 315 320

Leu Leu Val Leu Ser Gly Val Val Met Val Phe Ser Thr Ser Ala Phe
 325 330 335

Gly Ala Tyr Phe Lys Leu Thr Gln Gly Gly Pro Gly Asn Ser Ser His
 340 345 350

Val Ala Ile Ser Ala Pro Val Ser Ala Gln Pro Val Asp Ala Ser Val
 355 360 365

Gly Leu Ala Trp Leu Ala Val Gly Ser Met Cys Leu Phe Ile Ala Gly
 370 375 380

Phe Ala Val Gly Trp Gly Pro Ile Pro Trp Leu Leu Met Ser Glu Ile
 385 390 395 400

Phe Pro Leu His Val Lys Gly Val Ala Thr Gly Ile Cys Val Leu Thr
 405 410 415

Asn Trp Leu Met Ala Phe Leu Val Thr Lys Glu Phe Ser Ser Leu Met
 420 425 430

Glu Val Leu Arg Pro Tyr Gly Ala Phe Trp Leu Ala Ser Ala Phe Cys
 435 440 445

Ile Phe Ser Val Leu Phe Thr Phe Ser Cys Val Pro Glu Thr Lys Gly

450	455	460	
Lys Thr Leu Glu Gln Ile Thr Ala His Phe Glu Gly Arg			
465	470	475	
<p><210> 49</p> <p><211> 1863</p> <p><212> DNA</p> <p><213> GLUT9</p> <p><220></p> <p><221> . CDS</p> <p><222> (55)..(1677)</p> <p><223></p> <p><400> 49</p>			
cttggcagag tctgggggtcc ctggactgag ccatcagctg ggtcactgag accc atg			57
			Met
			1
gca agg aaa caa aat agg aat tcc aag gaa ctg ggc cta gtt ccc ctc			105
Ala Arg Lys Gln Asn Arg Asn Ser Lys Glu Leu Gly Leu Val Pro Leu			
	5	10	15
aca gat gac acc agc cac gcc agg cct cca ggg cca ggg agg gca ctg			153
Thr Asp Asp Thr Ser His Ala Arg Pro Pro Gly Pro Gly Arg Ala Leu			
	20	25	30
ctg gag tgt gac cac ctg agg agt ggg gtg cca ggt gga agg aga aga			201
Leu Glu Cys Asp His Leu Arg Ser Gly Val Pro Gly Gly Arg Arg Arg			
	35	40	45
aag gac tgg tcc tgc tcg ctc ctc gtg gcc tcc ctc gcg ggc gcc ttc			249
Lys Asp Trp Ser Cys Ser Leu Leu Val Ala Ser Leu Ala Gly Ala Phe			
	50	55	60
ggc tcc tcc ttc ctc tac ggc tac aac ctg tcg gtg gtg aat gcc ccc			297
Gly Ser Ser Phe Leu Tyr Gly Tyr Asn Leu Ser Val Val Asn Ala Pro			
	70	75	80
acc ccg tac atc aag gcc ttt tac aat gag tca tgg gaa aga agg cat			345
Thr Pro Tyr Ile Lys Ala Phe Tyr Asn Glu Ser Trp Glu Arg Arg His			
	85	90	95
gga cgt cca ata gac cca gac act ctg act ctg ctc tgg tct gtg act			393
Gly Arg Pro Ile Asp Pro Asp Thr Leu Thr Leu Leu Trp Ser Val Thr			
	100	105	110
gtg tcc ata ttc gcc atc ggt gga ctt gtg ggg aca tta att gtg aag			441
Val Ser Ile Phe Ala Ile Gly Gly Leu Val Gly Thr Leu Ile Val Lys			
	115	120	125
atg att gga aag gtt ctt ggg agg aag cac act ttg ctg gcc aat aat			489
Met Ile Gly Lys Val Leu Gly Arg Lys His Thr Leu Leu Ala Asn Asn			
	130	135	140
ggg ttt gca att tct gct gca ttg ctg atg gcc tgc tcg ctc cag gca			537
Gly Phe Ala Ile Ser Ala Ala Leu Leu Met Ala Cys Ser Leu Gln Ala			
	150	155	160
gga gcc ttt gaa atg ctc atc gtg gga cgc ttc atc atg ggc ata gat			585

Gly	Ala	Phe	Glu	Met	Leu	Ile	Val	Gly	Arg	Phe	Ile	Met	Gly	Ile	Asp	
			165					170					175			
gga	ggc	gtc	gcc	ctc	agt	gtg	ctc	ccc	atg	tac	ctc	agt	gag	atc	tca	633
Gly	Gly	Val	Ala	Leu	Ser	Val	Leu	Pro	Met	Tyr	Leu	Ser	Glu	Ile	Ser	
		180					185					190				
ccc	aag	gag	atc	cgt	ggc	tct	ctg	ggg	cag	gtg	act	gcc	atc	ttt	atc	681
Pro	Lys	Glu	Ile	Arg	Gly	Ser	Leu	Gly	Gln	Val	Thr	Ala	Ile	Phe	Ile	
	195					200					205					
tgc	att	ggc	gtg	ttc	act	ggg	cag	ctt	ctg	ggc	ctg	ccc	gag	ctg	ctg	729
Cys	Ile	Gly	Val	Phe	Thr	Gly	Gln	Leu	Leu	Gly	Leu	Pro	Glu	Leu	Leu	
210					215					220					225	
gga	aag	gag	agt	acc	tgg	cca	tac	ctg	ttt	gga	gtg	att	gtg	gtc	cct	777
Gly	Lys	Glu	Ser	Thr	Trp	Pro	Tyr	Leu	Phe	Gly	Val	Ile	Val	Val	Pro	
				230					235					240		
gcc	gtt	gtc	cag	ctg	ctg	agc	ctt	ccc	ttt	ctc	ccg	gac	agc	cca	cgc	825
Ala	Val	Val	Gln	Leu	Leu	Ser	Leu	Pro	Phe	Leu	Pro	Asp	Ser	Pro	Arg	
			245					250					255			
tac	ctg	ctc	ttg	gag	aag	cac	aac	gag	gca	aga	gct	gtg	aaa	gcc	ttc	873
Tyr	Leu	Leu	Leu	Glu	Lys	His	Asn	Glu	Ala	Arg	Ala	Val	Lys	Ala	Phe	
		260					265					270				
caa	acg	ttc	ttg	ggc	aaa	gca	gac	gtt	tcc	caa	gag	gta	gag	gag	gtc	921
Gln	Thr	Phe	Leu	Gly	Lys	Ala	Asp	Val	Ser	Gln	Glu	Val	Glu	Glu	Val	
	275					280					285					
ctg	gct	gag	agc	cgc	gtg	cag	agg	agc	atc	cgc	ctg	gtg	tcc	gtg	ctg	969
Leu	Ala	Glu	Ser	Arg	Val	Gln	Arg	Ser	Ile	Arg	Leu	Val	Ser	Val	Leu	
290					295					300					305	
gag	ctg	ctg	aga	gct	ccc	tac	gtc	cgc	tgg	cag	gtg	gtc	acc	gtg	att	1017
Glu	Leu	Leu	Arg	Ala	Pro	Tyr	Val	Arg	Trp	Gln	Val	Val	Thr	Val	Ile	
				310					315					320		
gtc	acc	atg	gcc	tgc	tac	cag	ctc	tgt	ggc	ctc	aat	gca	att	tgg	ttc	1065
Val	Thr	Met	Ala	Cys	Tyr	Gln	Leu	Cys	Gly	Leu	Asn	Ala	Ile	Trp	Phe	
			325					330					335			
tat	acc	aac	agc	atc	ttt	gga	aaa	gct	ggg	atc	cct	ctg	gca	aag	atc	1113
Tyr	Thr	Asn	Ser	Ile	Phe	Gly	Lys	Ala	Gly	Ile	Pro	Leu	Ala	Lys	Ile	
		340					345					350				
cca	tac	gtc	acc	ttg	agt	aca	ggg	ggc	atc	gag	act	ttg	gct	gcc	gtc	1161
Pro	Tyr	Val	Thr	Leu	Ser	Thr	Gly	Gly	Ile	Glu	Thr	Leu	Ala	Ala	Val	
		355				360					365					
ttc	tct	ggc	ttg	gtc	att	gag	cac	ctg	gga	cgg	aga	ccc	ctc	ctc	att	1209
Phe	Ser	Gly	Leu	Val	Ile	Glu	His	Leu	Gly	Arg	Arg	Pro	Leu	Leu	Ile	
370					375					380					385	
ggc	ggc	ttt	ggg	ctc	atg	ggc	ctc	ttc	ttt	ggg	acc	ctc	acc	atc	acg	1257
Gly	Gly	Phe	Gly	Leu	Met	Gly	Leu	Phe	Phe	Gly	Thr	Leu	Thr	Ile	Thr	
				390					395					400		
ctg	acc	ctg	cag	gac	cac	gcc	ccc	tgg	gtc	ccc	tac	ctg	agt	atc	gtg	1305
Leu	Thr	Leu	Gln	Asp	His	Ala	Pro	Trp	Val	Pro	Tyr	Leu	Ser	Ile	Val	
			405					410						415		

ggc att ctg gcc atc atc gcc tct ttc tgc agt ggg cca ggt ggc atc 1353
 Gly Ile Leu Ala Ile Ile Ala Ser Phe Cys Ser Gly Pro Gly Gly Ile
 420 425 430

ccg ttc atc ttg act ggt gag ttc ttc cag caa tct cag cgg ccg gct 1401
 Pro Phe Ile Leu Thr Gly Glu Phe Phe Gln Gln Ser Gln Arg Pro Ala
 435 440 445

gcc ttc atc att gca ggc acc gtc aac tgg ctc tcc aac ttt gct gtt 1449
 Ala Phe Ile Ile Ala Gly Thr Val Asn Trp Leu Ser Asn Phe Ala Val
 450 455 460 465

ggg ctc ctc ttc cca ttc att cag aaa agt ctg gac acc tac tgt ttc 1497
 Gly Leu Leu Phe Pro Phe Ile Gln Lys Ser Leu Asp Thr Tyr Cys Phe
 470 475 480

cta gtc ttt gct aca att tgt atc aca ggt gct atc tac ctg tat ttt 1545
 Leu Val Phe Ala Thr Ile Cys Ile Thr Gly Ala Ile Tyr Leu Tyr Phe
 485 490 495

gtg ctg cct gag acc aaa aac aga acc tat gca gaa atc agc cag gca 1593
 Val Leu Pro Glu Thr Lys Asn Arg Thr Tyr Ala Glu Ile Ser Gln Ala
 500 505 510

ttt tcc aaa agg aac aaa gca tac cca cca gaa gag aaa atc gac tca 1641
 Phe Ser Lys Arg Asn Lys Ala Tyr Pro Pro Glu Glu Lys Ile Asp Ser
 515 520 525

gct gtc act gat ggt aag ata aat gga agg cct taa caagtttcct 1687
 Ala Val Thr Asp Gly Lys Ile Asn Gly Arg Pro
 530 535 540

cctccacgtt ggacaattat gtcaaaaaca ggattgtcta catggatgat ctcaacttttc 1747

aggaaactta aaatttaccc attattggga agcttaaagct aattgaagct atgcaagtct 1807

tttatattat taaatattta aaagtaaacc tgtactaatc taaaaaaaaa aaaaaa 1863

<210> 50
 <211> 540
 <212> PRT
 <213> GLUT9

<400> 50

Met Ala Arg Lys Gln Asn Arg Asn Ser Lys Glu Leu Gly Leu Val Pro
 1 5 10 15

Leu Thr Asp Asp Thr Ser His Ala Arg Pro Pro Gly Pro Gly Arg Ala
 20 25 30

Leu Leu Glu Cys Asp His Leu Arg Ser Gly Val Pro Gly Gly Arg Arg
 35 40 45

Arg Lys Asp Trp Ser Cys Ser Leu Leu Val Ala Ser Leu Ala Gly Ala
 50 55 60

Phe Gly Ser Ser Phe Leu Tyr Gly Tyr Asn Leu Ser Val Val Asn Ala

97

65		70		75		80
Pro Thr Pro Tyr	Ile Lys Ala Phe Tyr	Asn Glu Ser Trp	Glu Arg Arg			
	85	90	95			
His Gly Arg Pro	Ile Asp Pro Asp	Thr Leu Thr Leu	Leu Trp Ser Val			
	100	105	110			
Thr Val Ser Ile	Phe Ala Ile Gly	Gly Leu Val Gly	Thr Leu Ile Val			
	115	120	125			
Lys Met Ile Gly	Lys Val Leu Gly	Arg Lys His Thr	Leu Leu Ala Asn			
	130	135	140			
Asn Gly Phe Ala	Ile Ser Ala Ala	Leu Leu Met Ala	Cys Ser Leu Gln			
	145	150	155	160		
Ala Gly Ala Phe	Glu Met Leu Ile	Val Gly Arg Phe	Ile Met Gly Ile			
	165	170	175			
Asp Gly Gly Val	Ala Leu Ser Val	Leu Pro Met Tyr	Leu Ser Glu Ile			
	180	185	190			
Ser Pro Lys Glu	Ile Arg Gly Ser	Leu Gly Gln Val	Thr Ala Ile Phe			
	195	200	205			
Ile Cys Ile Gly	Val Phe Thr Gly	Gln Leu Leu Gly	Leu Pro Glu Leu			
	210	215	220			
Leu Gly Lys Glu	Ser Thr Trp Pro	Tyr Leu Phe Gly	Val Ile Val Val			
	225	230	235	240		
Pro Ala Val Val	Gln Leu Leu Ser	Leu Pro Phe Leu	Pro Asp Ser Pro			
	245	250	255			
Arg Tyr Leu Leu	Leu Glu Lys His	Asn Glu Ala Arg	Ala Val Lys Ala			
	260	265	270			
Phe Gln Thr Phe	Leu Gly Lys Ala	Asp Val Ser Gln	Glu Val Glu Glu			
	275	280	285			
Val Leu Ala Glu	Ser Arg Val Gln	Arg Ser Ile Arg	Leu Val Ser Val			
	290	295	300			
Leu Glu Leu Leu	Arg Ala Pro Tyr	Val Arg Trp Gln	Val Val Thr Val			
	305	310	315	320		

98

Ile Val Thr Met Ala Cys Tyr Gln Leu Cys Gly Leu Asn Ala Ile Trp
 325 330 335

Phe Tyr Thr Asn Ser Ile Phe Gly Lys Ala Gly Ile Pro Leu Ala Lys
 340 345 350

Ile Pro Tyr Val Thr Leu Ser Thr Gly Gly Ile Glu Thr Leu Ala Ala
 355 360 365

Val Phe Ser Gly Leu Val Ile Glu His Leu Gly Arg Arg Pro Leu Leu
 370 375 380

Ile Gly Gly Phe Gly Leu Met Gly Leu Phe Phe Gly Thr Leu Thr Ile
 385 390 395 400

Thr Leu Thr Leu Gln Asp His Ala Pro Trp Val Pro Tyr Leu Ser Ile
 405 410 415

Val Gly Ile Leu Ala Ile Ile Ala Ser Phe Cys Ser Gly Pro Gly Gly
 420 425 430

Ile Pro Phe Ile Leu Thr Gly Glu Phe Phe Gln Gln Ser Gln Arg Pro
 435 440 445

Ala Ala Phe Ile Ile Ala Gly Thr Val Asn Trp Leu Ser Asn Phe Ala
 450 455 460

Val Gly Leu Leu Phe Pro Phe Ile Gln Lys Ser Leu Asp Thr Tyr Cys
 465 470 475 480

Phe Leu Val Phe Ala Thr Ile Cys Ile Thr Gly Ala Ile Tyr Leu Tyr
 485 490 495

Phe Val Leu Pro Glu Thr Lys Asn Arg Thr Tyr Ala Glu Ile Ser Gln
 500 505 510

Ala Phe Ser Lys Arg Asn Lys Ala Tyr Pro Pro Glu Glu Lys Ile Asp
 515 520 525

Ser Ala Val Thr Asp Gly Lys Ile Asn Gly Arg Pro
 530 535 540

<210> 51
 <211> 4167
 <212> DNA
 <213> GLUT10

<220>
 <221> CDS

<222> (53)..(1678)

<223>

<400> 51

atgcgcgccc ggccccctcag cgccccccagc acgcccgcga gtcccgcctcg cc atg ggc	58
Met Gly	
1	
 cac tcc cca cct gtc ctg cct ttg tgt gcc tct gtg tct ttg ctg ggt	106
His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val Ser Leu Leu Gly	
5 10 15	
 ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca ggt gcc ctg ctg	154
Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser Gly Ala Leu Leu	
20 25 30	
 cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag cag gag ttc ctg	202
Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu Gln Glu Phe Leu	
35 40 45 50	
 gtg ggc agc ctg ctc ctg ggg gct ctc ctc gcc tcc ctg gtt ggt ggc	250
Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser Leu Val Gly Gly	
55 60 65	
 ttc ctc att gac tgc tat ggc agg aag caa gcc atc ctc ggg agc aac	298
Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly Ser Asn	
70 75 80	
 ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg gct ggt tcc ctg	346
Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly Ser Leu	
85 90 95	
 gcc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc gcc att tcc ctc	394
Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile Ser Leu	
100 105 110	
 tcc tcc atg gct tgc tgt atc tac gtg tca gag ctg gtg ggg cca cgg	442
Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly Pro Arg	
115 120 125 130	
 cag cgg gga gtg ctg gtg tcc ctc tat gag gca ggc atc acc gtg ggc	490
Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr Val Gly	
135 140 145	
 atc ctg ctc tcc tat gcc ctc aac tat gca ctg gct ggt acc ccc tgg	538
Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr Pro Trp	
150 155 160	
 gga tgg agg cac atg ttc ggc tgg gcc act gca cct gct gtc ctg caa	586
Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro Ala Val Leu Gln	
165 170 175	
 tcc ctc agc ctc ctc ttc ctc cct gct ggt aca gat gag act gca aca	634
Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp Glu Thr Ala Thr	
180 185 190	
 cac aag gac ctc atc cca ctc cag gga ggt gag gcc ccc aag ctg ggc	682
His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys Leu Gly	
195 200 205 210	
 ccg ggg agg cca cgg tac tcc ttt ctg gac ctc ttc agg gca cgc gat	730
Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala Arg Asp	
215 220 225	

100

aac atg cga ggc cgg acc aca gtg ggc ctg ggg ctg gtg ctc ttc cag Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu Phe Gln 230 235 240	778
caa cta aca ggg cag ccc aac gtg ctg tgc tat gcc tcc acc atc ttc Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr Ile Phe 245 250 255	826
agc tcc gtt ggt ttc cat ggg gga tcc tca gcc gtg ctg gcc tct gtg Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala Ser Val 260 265 270	874
ggg ctt ggc gca gtg aag gtg gca gct acc ctg acc gcc atg ggg ctg Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met Gly Leu 275 280 285 290	922
gtg gac cgt gca ggc cgc agg gct ctg ttg cta gct ggc tgt gcc ctc Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys Ala Leu 295 300 305	970
atg gcc ctg tcc gtc agt ggc ata ggc ctc gtc agc ttt gcc gtg ccc Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala Val Pro 310 315 320	1018
atg gac tca ggc cca agc tgt ctg gct gtg ccc aat gcc acc ggg cag Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr Gly Gln 325 330 335	1066
aca ggc ctc cct gga gac tct ggc ctg ctg cag gac tcc tct cta cct Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser Leu Pro 340 345 350	1114
ccc att cca agg acc aat gag gac caa agg gag cca atc ttg tcc act Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu Ser Thr 355 360 365 370	1162
gct aag aaa acc aag ccc cat ccc aga tct gga gac ccc tca gcc cct Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser Ala Pro 375 380 385	1210
cct cgg ctg gcc ctg agc tct gcc ctc cct ggg ccc cct ctg ccc gct Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu Pro Ala 390 395 400	1258
cgg ggg cat gca ctg ctg cgc tgg acc gca ctg ctg tgc ctg atg gtc Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu Met Val 405 410 415	1306
ttt gtc agt gcc ttc tcc ttt ggg ttt ggg cca gtg acc tgg ctt gtc Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp Leu Val 420 425 430	1354
ctc agc gag atc tac cct gtg gag ata cga gga aga gcc ttc gcc ttc Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe Ala Phe 435 440 445 450	1402
tgc aac agc ttc aac tgg gcg gcc aac ctc ttc atc agc ctc tcc ttc Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu Ser Phe 455 460 465	1450
ctc gat ctc att ggc acc atc ggc ttg tcc tgg acc ttc ctg ctc tac Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu Leu Tyr	1498

470	475	480	
gga ctg acc gct gtc ctc ggc ctg ggc ttc atc tat tta ttt gtt cct			1546
Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe Val Pro			
485	490	495	
gaa aca aaa ggc cag tgc ttg gca gag ata gac cag cag ttc cag aag			1594
Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe Gln Lys			
500	505	510	
aga cgg ttc acc ctg agc ttt ggc cac agg cag aac tcc act ggc atc			1642
Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr Gly Ile			
515	520	525	530
ccg tac agc cgc atc gag atc tct gcg gcc tcc tga ggaatccgctc			1688
Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser			
535	540		
tgccctgaaa ttctggaact gtggctttgg cagaccatct ccagcatcct gcttcctagg			1748
ccccagagca caagttccag ctgggtctttt gggagtggcc cctgccccca aagggtgtct			1808
gcttttgctg gggtaaaaag gatgaaagtc tgagaatgcc caactcttca ttttgagtct			1868
caggccctga aggttcctga ggatctagct tcatgcctca gtttccccat tgacttgcac			1928
atctctgcag tatttataag aagaatattc tatgaagtct ttgttgacc atggactttt			1988
ctcaaagaat ctcaagggtg ccaatcctgg caggaagtct ctcccgatat caccctaaa			2048
tccaaatgag gatatcatct tttctaactc cttttttcaa ctggctggga cattttcgga			2108
agggggaagt ctcttttttt actcttatca tttttttttt ttgaggtgga gtctcattct			2168
gttgcccagg ctggcctgat cttggctcac tgcaacctcc acctcctgag ttcaagcgat			2228
tcttgtgcct cagcctccta agcagctggg actacaggcg catgcaacca taccagcta			2288
atatttttt agcagagatg gggtttcaact gtgttgcca ggctggtcgt gaactcctga			2348
gctcaagtga tccaccacc tcagcctccc agagtgctag gattacaggc cttttgactc			2408
ttttatctga gttttattga cccctctaata tctcttacct agaataattta tccttcacca			2468
gcaactctga ctctttgacg ggaggcctca gttctagtcc ttggtctgct ggtgtcattg			2528
ctgtaggaat gaccacgggc ctgagtttcc ccatattgtat aatgggaagc ctgtaccagg			2588
tcattcttaa gattttctct gactccagtg agctggaatt ctaaatgctg gtctaggagc			2648
tgtctccagg atggtgcagg atggctttgc ggaaaggaga tgggtttgga ggccaacaaa			2708
cctgcttgtc aatattgcct ttgcctcttg gcagcccttg aacttgagta aataacaact			2768
ccctgaacct cagtttctc atctgcagaa tggggataat tatgtcccag gggatatatt			2828
agaccctgtt tcctttcagg agggccccca gctggtccag ggccctgggaa atttctactt			2888
atcctcatta cccaggtccc tcctttggac cctgtaaagg gtcagggtga atcagatggg			2948
ggactgagca agtagctatg actgcagatc atgtaaggaa gggactgaca agaagctccc			3008
agatgctggg gagaatgaag agctaaaata gatcctaggt gctggatgct ttgtcatcca			3068

102

tgcgtgcaca tatgggtgct ggcagagccc ccaaggactc tggcctctcg agttctccta 3128
 tcttctccat tctagatgct tcccttgtat ccagtgatgt gctggagctg gctttgccaa 3188
 gcttgtgaga gctgggttgct acattttcag gatttttaca agttggtaaa cacagccatt 3248
 ataaaaaatt aaatgattta aattttataat taagtaaatt acattaaaac aaaaaaatta 3308
 tactcaaaat tcattactta attttactac ctgttactat tatctgtgct tttgaggcta 3368
 tttctacata gtaactctta tggagaccta ggggagacac cgcgcatctc ttcctgatcc 3428
 cccactcaat gacatcatgt tagtctttgg ttgcttaact ggctgtgggg agtggttttg 3488
 tatcacaag attagagagg actacacatc agggcttgat ttattgtttg ttgattttct 3548
 agacttcaga acatgctgga taaaatgtca gtaatgcaa ttaaacttta aagtatgtct 3608
 tgtttgtagc caatacatgg tgtatagcac caaaaaatgg agggattatt cttccagtag 3668
 ttgaacactg tcatccgttt cagctgacag ctgctcaaat catttaagaa ggagttctga 3728
 cattcatttt cattgtttta cttttgtctt cctcactagt gtaaacaaaa atttcaacca 3788
 gcattcatgc cgaacctata cccattcttc agtgcctagc tgtacagtta tcagggattt 3848
 ttattttgtag tctaattttg tcaaatcatg gccaaatcgc agtgatagtt gactttggat 3908
 acaaggtttg gcaaaaaaaaa aaatattaac aaaatattct gtaagaatca attgtctata 3968
 tggaatttag gataaagaat attacaata aagaatattt acaataaaga gtttattatt 4028
 atttgtaagt tgtgtgcaac aaacataccc tttatctctg taaaatttat acacacaaaa 4088
 attaacaaaa gattctgtaa gaattaattg gctatatgga atttaggata gaatatttac 4148
 aataaagagt atttacaat 4167

<210> 52
 <211> 541
 <212> PRT
 <213> GLUT10

<400> 52

Met Gly His Ser Pro Pro Val Leu Pro Leu Cys Ala Ser Val Ser Leu
 1 5 10 15

Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser Gly Ala
 20 25 30

Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu Gln Glu
 35 40 45

Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser Leu Val
 50 55 60

103

Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly
 65 70 75 80

Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly
 85 90 95

Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile
 100 105 110

Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly
 115 120 125

Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr
 130 135 140

Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr
 145 150 155 160

Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro Ala Val
 165 170 175

Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp Glu Thr
 180 185 190

Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys
 195 200 205

Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala
 210 215 220

Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu
 225 230 235 240

Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr
 245 250 255

Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala
 260 265 270

Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met
 275 280 285

Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys
 290 295 300

Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser Phe Ala
 305 310 315 320

104

Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr
 325 330 335
 Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser
 340 345 350
 Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu
 355 360 365
 Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser
 370 375 380
 Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu
 385 390 395 400
 Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu
 405 410 415
 Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp
 420 425 430
 Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe
 435 440 445
 Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu
 450 455 460
 Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu
 465 470 475 480
 Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe
 485 490 495
 Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe
 500 505 510
 Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr
 515 520 525
 Gly Ile Pro Tyr Ser Arg Ile Glu Ile Ser Ala Ala Ser
 530 535 540

<210> 53
 <211> 1608
 <212> DNA
 <213> GLUT11

<220>

105

```

<221> CDS
<222> (100)..(1590)
<223>

<400> 53
cggacctgcc tctcacgcaa tggatcccct ggcggcaacc cgagaccggt tctcctaccc      60

gcattccgcc aagtctctcg ctctgccag gacgcacag atg aga gcg ctc cga      114
                               Met Arg Ala Leu Arg
                               1           5

aga ctg att cag ggc agg atc ctg ctc ctg acc atc tgc gct gcc ggc      162
Arg Leu Ile Gln Gly Arg Ile Leu Leu Thr Ile Cys Ala Ala Gly
                10                15                20

att ggt ggg act ttt cag ttt ggc tat aac ctc tct atc atc aat gcc      210
Ile Gly Gly Thr Phe Gln Phe Gly Tyr Asn Leu Ser Ile Ile Asn Ala
                25                30                35

ccg acc ttg cac att cag gaa ttc acc aat gag aca tgg cag gcg cgt      258
Pro Thr Leu His Ile Gln Glu Phe Thr Asn Glu Thr Trp Gln Ala Arg
                40                45                50

act gga gag cca ctg ccc gat cac cta gtc ctg ctt atg tgg tcc ctc      306
Thr Gly Glu Pro Leu Pro Asp His Leu Val Leu Leu Met Trp Ser Leu
                55                60                65

atc gtg tct ctg tat ccc ctg gga ggc ctc ttt gga gca ctg ctt gca      354
Ile Val Ser Leu Tyr Pro Leu Gly Gly Leu Phe Gly Ala Leu Leu Ala
                70                75                80                85

ggg ccc ttg gcc atc acg ctg gga agg aag aag tcc ctc ctg gtg aat      402
Gly Pro Leu Ala Ile Thr Leu Gly Arg Lys Lys Ser Leu Leu Val Asn
                90                95                100

aac atc ttt gtg gtg tca gca gca atc ctg ttt gga ttc agc cgc aaa      450
Asn Ile Phe Val Val Ser Ala Ala Ile Leu Phe Gly Phe Ser Arg Lys
                105                110                115

gca ggc tcc ttt gag atg atc atg ctg gga aga ctg ctc gtg gga gtc      498
Ala Gly Ser Phe Glu Met Ile Met Leu Gly Arg Leu Leu Val Gly Val
                120                125                130

aat gca ggt gtg agc atg aac atc cag ccc atg tac ctg ggg gag agc      546
Asn Ala Gly Val Ser Met Asn Ile Gln Pro Met Tyr Leu Gly Glu Ser
                135                140                145

gcc cct aag gag ctc cga gga gct gtg gcc atg agc tca gcc atc ttt      594
Ala Pro Lys Glu Leu Arg Gly Ala Val Ala Met Ser Ser Ala Ile Phe
                150                155                160                165

acg gct ctg ggg atc gtg atg gga cag gtg gtc gga ctc agg gag ctc      642
Thr Ala Leu Gly Ile Val Met Gly Gln Val Val Gly Leu Arg Glu Leu
                170                175                180

cta ggt ggc cct cag gcc tgg ccc ctg ctg ctg gcc agc tgc ctg gtg      690
Leu Gly Gly Pro Gln Ala Trp Pro Leu Leu Leu Ala Ser Cys Leu Val
                185                190                195

ccc ggg gcg ctc cag ctc gcc tcc ctg cct ctg ctc cct gaa agc ccg      738
Pro Gly Ala Leu Gln Leu Ala Ser Leu Pro Leu Leu Pro Glu Ser Pro
                200                205                210

```

cgc tac ctc ctc att gac tgt gga gac acc gag gcc tgc ctg gca gca Arg Tyr Leu Leu Ile Asp Cys Gly Asp Thr Glu Ala Cys Leu Ala Ala 215 220 225	786
cta cgg cgg ctc cgg ggc tcc ggg gac ttg gca ggg gag ctg gag gag Leu Arg Arg Leu Arg Gly Ser Gly Asp Leu Ala Gly Glu Leu Glu Glu 230 235 240 245	834
ctg gag gag gag cgc gct gcc tgc cag ggc tgc cgt gcc cgg cgc cca Leu Glu Glu Glu Arg Ala Ala Cys Gln Gly Cys Arg Ala Arg Arg Pro 250 255 260	882
tgg gag ctg ttc cag cat cgg gcc ctg agg aga cag gtg aca agc ctc Trp Glu Leu Phe Gln His Arg Ala Leu Arg Arg Gln Val Thr Ser Leu 265 270 275	930
gtg gtt ctg ggc agt gcc atg gag ctc tgc ggg aat gac tcg gtg tac Val Val Leu Gly Ser Ala Met Glu Leu Cys Gly Asn Asp Ser Val Tyr 280 285 290	978
gcc tac gcc tcc tcc gtg ttc cgg aag gca gga gtg ccg gaa gcg aag Ala Tyr Ala Ser Ser Val Phe Arg Lys Ala Gly Val Pro Glu Ala Lys 295 300 305	1026
atc cag tac gcg atc atc ggg act ggg agc tgc gag ctg ctc acg gcg Ile Gln Tyr Ala Ile Ile Gly Thr Gly Ser Cys Glu Leu Leu Thr Ala 310 315 320 325	1074
gtt gtt agt tgt gtg gta atc gag agg gtg ggt cgg cgc gtg ctg ctc Val Val Ser Cys Val Val Ile Glu Arg Val Gly Arg Arg Val Leu Leu 330 335 340	1122
atc ggt ggg tac agc ctg atg acc tgc tgg ggg agc atc ttc act gtg Ile Gly Gly Tyr Ser Leu Met Thr Cys Trp Gly Ser Ile Phe Thr Val 345 350 355	1170
gcc ctg tgc ctg cag agc tcc ttc ccc tgg aca ctc tac ctg gcc atg Ala Leu Cys Leu Gln Ser Ser Phe Pro Trp Thr Leu Tyr Leu Ala Met 360 365 370	1218
gcc tgc atc ttt gcc ttc atc ctc agc ttt ggc att ggc cct gcc gga Ala Cys Ile Phe Ala Phe Ile Leu Ser Phe Gly Ile Gly Pro Ala Gly 375 380 385	1266
gtg acg ggg atc ctg gcc aca gag ctg ttt gac cag atg gcc agg cct Val Thr Gly Ile Leu Ala Thr Glu Leu Phe Asp Gln Met Ala Arg Pro 390 395 400 405	1314
gct gcc tgc atg gtc tgc ggg gcg ctc atg tgg atc atg ctc atc ctg Ala Ala Cys Met Val Cys Gly Ala Leu Met Trp Ile Met Leu Ile Leu 410 415 420	1362
gtc ggc ctg gga ttt ccc ttt atc atg gag gcc ttg tcc cac ttc ctc Val Gly Leu Gly Phe Pro Phe Ile Met Glu Ala Leu Ser His Phe Leu 425 430 435	1410
tat gtc cct ttc ctt ggt gtc tgt gtc tgt ggg gcc atc tac act ggc Tyr Val Pro Phe Leu Gly Val Cys Val Cys Gly Ala Ile Tyr Thr Gly 440 445 450	1458
ctg ttc ctt cct gag acc aaa ggc aag acc ttc caa gag atc tcc aag Leu Phe Leu Pro Glu Thr Lys Gly Lys Thr Phe Gln Glu Ile Ser Lys 455 460 465	1506

107

gaa tta cac aga ctc aac ttc ccc agg cgg gcc cag ggc ccc acg tgg 1554
 Glu Leu His Arg Leu Asn Phe Pro Arg Arg Ala Gln Gly Pro Thr Trp
 470 475 480 485

agg agc ctg gag gtt atc cag tca aca gaa ctc tag tcccaaaggg 1600
 Arg Ser Leu Glu Val Ile Gln Ser Thr Glu Leu
 490 495

gtggccag 1608

<210> 54
 <211> 496
 <212> PRT
 <213> GLUT11

<400> 54

Met Arg Ala Leu Arg Arg Leu Ile Gln Gly Arg Ile Leu Leu Leu Thr
 1 5 10 15

Ile Cys Ala Ala Gly Ile Gly Gly Thr Phe Gln Phe Gly Tyr Asn Leu
 20 25 30

Ser Ile Ile Asn Ala Pro Thr Leu His Ile Gln Glu Phe Thr Asn Glu
 35 40 45

Thr Trp Gln Ala Arg Thr Gly Glu Pro Leu Pro Asp His Leu Val Leu
 50 55 60

Leu Met Trp Ser Leu Ile Val Ser Leu Tyr Pro Leu Gly Gly Leu Phe
 65 70 75 80

Gly Ala Leu Leu Ala Gly Pro Leu Ala Ile Thr Leu Gly Arg Lys Lys
 85 90 95

Ser Leu Leu Val Asn Asn Ile Phe Val Val Ser Ala Ala Ile Leu Phe
 100 105 110

Gly Phe Ser Arg Lys Ala Gly Ser Phe Glu Met Ile Met Leu Gly Arg
 115 120 125

Leu Leu Val Gly Val Asn Ala Gly Val Ser Met Asn Ile Gln Pro Met
 130 135 140

Tyr Leu Gly Glu Ser Ala Pro Lys Glu Leu Arg Gly Ala Val Ala Met
 145 150 155 160

Ser Ser Ala Ile Phe Thr Ala Leu Gly Ile Val Met Gly Gln Val Val
 165 170 175

108

Gly Leu Arg Glu Leu Leu Gly Gly Pro Gln Ala Trp Pro Leu Leu Leu
 180 185 190

Ala Ser Cys Leu Val Pro Gly Ala Leu Gln Leu Ala Ser Leu Pro Leu
 195 200 205

Leu Pro Glu Ser Pro Arg Tyr Leu Leu Ile Asp Cys Gly Asp Thr Glu
 210 215 220

Ala Cys Leu Ala Ala Leu Arg Arg Leu Arg Gly Ser Gly Asp Leu Ala
 225 230 235 240

Gly Glu Leu Glu Glu Leu Glu Glu Glu Arg Ala Ala Cys Gln Gly Cys
 245 250 255

Arg Ala Arg Arg Pro Trp Glu Leu Phe Gln His Arg Ala Leu Arg Arg
 260 265 270

Gln Val Thr Ser Leu Val Val Leu Gly Ser Ala Met Glu Leu Cys Gly
 275 280 285

Asn Asp Ser Val Tyr Ala Tyr Ala Ser Ser Val Phe Arg Lys Ala Gly
 290 295 300

Val Pro Glu Ala Lys Ile Gln Tyr Ala Ile Ile Gly Thr Gly Ser Cys
 305 310 315 320

Glu Leu Leu Thr Ala Val Val Ser Cys Val Val Ile Glu Arg Val Gly
 325 330 335

Arg Arg Val Leu Leu Ile Gly Gly Tyr Ser Leu Met Thr Cys Trp Gly
 340 345 350

Ser Ile Phe Thr Val Ala Leu Cys Leu Gln Ser Ser Phe Pro Trp Thr
 355 360 365

Leu Tyr Leu Ala Met Ala Cys Ile Phe Ala Phe Ile Leu Ser Phe Gly
 370 375 380

Ile Gly Pro Ala Gly Val Thr Gly Ile Leu Ala Thr Glu Leu Phe Asp
 385 390 395 400

Gln Met Ala Arg Pro Ala Ala Cys Met Val Cys Gly Ala Leu Met Trp
 405 410 415

Ile Met Leu Ile Leu Val Gly Leu Gly Phe Pro Phe Ile Met Glu Ala
 420 425 430

109

Leu Ser His Phe Leu Tyr Val Pro Phe Leu Gly Val Cys Val Cys Gly
 435 440 445

Ala Ile Tyr Thr Gly Leu Phe Leu Pro Glu Thr Lys Gly Lys Thr Phe
 450 455 460

Gln Glu Ile Ser Lys Glu Leu His Arg Leu Asn Phe Pro Arg Arg Ala
 465 470 475 480

Gln Gly Pro Thr Trp Arg Ser Leu Glu Val Ile Gln Ser Thr Glu Leu
 485 490 495

<210> 55
 <211> 2223
 <212> DNA
 <213> GLUT12

<220>
 <221> CDS
 <222> (106)..(1959)
 <223>

<400> 55
 acactcttct ttagcatgct attatgggga aagtgaccac tcctgggagc gggggtggtc 60
 ggggcggttt ggtggcgggg aagcggctgt aacttctacg tgacc atg gta cct gtt 117
 Met Val Pro Val
 1

gaa aac acc gag ggc ccc agt ctg ctg aac cag aag ggg aca gcc gtg 165
 Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys Gly Thr Ala Val
 5 10 15 20

gag acg gag ggc agc ggc agc cgg cat cct ccc tgg gcg aga ggc tgc 213
 Glu Thr Glu Gly Ser Gly Ser Arg His Pro Pro Trp Ala Arg Gly Cys
 25 30 35

ggc atg ttt acc ttc ctg tca tct gtc act gct gct gtc agt ggc ctc 261
 Gly Met Phe Thr Phe Leu Ser Ser Val Thr Ala Ala Val Ser Gly Leu
 40 45 50

ctg gtg ggt tat gaa ctt ggg atc atc tct ggg gct ctt ctt cag atc 309
 Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala Leu Leu Gln Ile
 55 60 65

aaa acc tta tta gcc ctg agc tgc cat gag cag gaa atg gtt gtg agc 357
 Lys Thr Leu Leu Ala Leu Ser Cys His Glu Gln Glu Met Val Val Ser
 70 75 80

tcc ctc gtc att gga gcc ctc ctt gcc tca ctc acc gga ggg gtc ctg 405
 Ser Leu Val Ile Gly Ala Leu Leu Ala Ser Leu Thr Gly Gly Val Leu
 85 90 95 100

ata gac aga tat gga aga agg aca gca atc atc ttg tca tcc tgc ctg 453
 Ile Asp Arg Tyr Gly Arg Arg Thr Ala Ile Ile Leu Ser Ser Cys Leu
 105 110 115

ctt gga ctc gga agc tta gtc ttg atc ctc agt tta tcc tac acg gtt 501

110

Leu Gly Leu Gly Ser Leu Val Leu Ile Leu Ser Leu Ser Tyr Thr Val	
120 125 130	
ctt ata gtg gga cgc att gcc ata ggg gtc tcc atc tcc ctc tct tcc	549
Leu Ile Val Gly Arg Ile Ala Ile Gly Val Ser Ile Ser Leu Ser Ser	
135 140 145	
att gcc act tgt gtt tac atc gca gag att gct cct caa cac aga aga	597
Ile Ala Thr Cys Val Tyr Ile Ala Glu Ile Ala Pro Gln His Arg Arg	
150 155 160	
ggc ctt ctt gtg tca ctg aat gag ctg atg att gtc atc ggc att ctt	645
Gly Leu Leu Val Ser Leu Asn Glu Leu Met Ile Val Ile Gly Ile Leu	
165 170 175 180	
tct gcc tat att tca aat tac gca ttt gcc aat gtt ttc cat ggc tgg	693
Ser Ala Tyr Ile Ser Asn Tyr Ala Phe Ala Asn Val Phe His Gly Trp	
185 190 195	
aag tac atg ttt ggt ctt gtg att ccc ttg gga gtt ttg caa gca att	741
Lys Tyr Met Phe Gly Leu Val Ile Pro Leu Gly Val Leu Gln Ala Ile	
200 205 210	
gca atg tat ttt ctt cct cca agc cct cgg ttt ctg gtg atg aaa gga	789
Ala Met Tyr Phe Leu Pro Pro Ser Pro Arg Phe Leu Val Met Lys Gly	
215 220 225	
caa gag gga gct gct agc aag gtt ctt gga agg tta aga gca ctc tca	837
Gln Glu Gly Ala Ala Ser Lys Val Leu Gly Arg Leu Arg Ala Leu Ser	
230 235 240	
gat aca act gag gaa ctc act gtg atc aaa tcc tcc ctg aaa gat gaa	885
Asp Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser Leu Lys Asp Glu	
245 250 255 260	
tat cag tac agt ttt tgg gat ctg ttt cgt tca aaa gac aac atg cgg	933
Tyr Gln Tyr Ser Phe Trp Asp Leu Phe Arg Ser Lys Asp Asn Met Arg	
265 270 275	
acc cga ata atg ata gga cta aca cta gta ttt ttt gta caa atc act	981
Thr Arg Ile Met Ile Gly Leu Thr Leu Val Phe Phe Val Gln Ile Thr	
280 285 290	
ggc caa cca aac ata ttg ttc tat gca tca act gtt ttg aag tca gtt	1029
Gly Gln Pro Asn Ile Leu Phe Tyr Ala Ser Thr Val Leu Lys Ser Val	
295 300 305	
gga ttt caa agc aat gag gca gct agc ctc gcc tcc act ggg gtt gga	1077
Gly Phe Gln Ser Asn Glu Ala Ala Ser Leu Ala Ser Thr Gly Val Gly	
310 315 320	
gtc gtc aag gtc att agc acc atc cct gcc act ctt ctt gta gac cat	1125
Val Val Lys Val Ile Ser Thr Ile Pro Ala Thr Leu Leu Val Asp His	
325 330 335 340	
gtt ggc agc aaa aca ttc ctc tgc att ggc tcc tct gtg atg gca gct	1173
Val Gly Ser Lys Thr Phe Leu Cys Ile Gly Ser Ser Val Met Ala Ala	
345 350 355	
tcg ttg gtg acc atg ggc atc gta aat ctc aac atc cac atg aac ttc	1221
Ser Leu Val Thr Met Gly Ile Val Asn Leu Asn Ile His Met Asn Phe	
360 365 370	

acc cat atc tgc aga agc cac aat tct atc aac cag tcc ttg gat gag	1269
Thr His Ile Cys Arg Ser His Asn Ser Ile Asn Gln Ser Leu Asp Glu	
375 380 385	
tct gtg att tat gga cca gga aac ctg tca acc aac aac aat act ctc	1317
Ser Val Ile Tyr Gly Pro Gly Asn Leu Ser Thr Asn Asn Asn Thr Leu	
390 395 400	
aga gac cac ttc aaa ggg att tct tcc cat agc aga agc tca ctc atg	1365
Arg Asp His Phe Lys Gly Ile Ser Ser His Ser Arg Ser Ser Leu Met	
405 410 415 420	
ccc ctg aga aat gat gtg gat aag aga ggg gag acg acc tca gca tcc	1413
Pro Leu Arg Asn Asp Val Asp Lys Arg Gly Glu Thr Thr Ser Ala Ser	
425 430 435	
ttg cta aat gct gga tta agc cac act gaa tac cag ata gtc aca gac	1461
Leu Leu Asn Ala Gly Leu Ser His Thr Glu Tyr Gln Ile Val Thr Asp	
440 445 450	
cct ggg gac gtc cca gct ttt ttg aaa tgg ctg tcc tta gcc agc ttg	1509
Pro Gly Asp Val Pro Ala Phe Leu Lys Trp Leu Ser Leu Ala Ser Leu	
455 460 465	
ctt gtt tat gtt gct gct ttt tca att ggt cta gga cca atg ccc tgg	1557
Leu Val Tyr Val Ala Ala Phe Ser Ile Gly Leu Gly Pro Met Pro Trp	
470 475 480	
ctg gtg ctc agc gag atc ttt cct ggt ggg atc aga gga cga gcc atg	1605
Leu Val Leu Ser Glu Ile Phe Pro Gly Gly Ile Arg Gly Arg Ala Met	
485 490 495 500	
gct tta act tct agc atg aac tgg ggc atc aat ctc ctc atc tcg ctg	1653
Ala Leu Thr Ser Ser Met Asn Trp Gly Ile Asn Leu Leu Ile Ser Leu	
505 510 515	
aca ttt ttg act gta act gat ctt att ggc ctg cca tgg gtg tgc ttt	1701
Thr Phe Leu Thr Val Thr Asp Leu Ile Gly Leu Pro Trp Val Cys Phe	
520 525 530	
ata tat aca atc atg agt cta gca tcc ctg ctt ttt gtt gtt atg ttt	1749
Ile Tyr Thr Ile Met Ser Leu Ala Ser Leu Leu Phe Val Val Met Phe	
535 540 545	
ata cct gag aca aag gga tgc tct ttg gaa caa ata tca atg gag cta	1797
Ile Pro Glu Thr Lys Gly Cys Ser Leu Glu Gln Ile Ser Met Glu Leu	
550 555 560	
gca aaa gtg aac tat gtg aaa aac aac att tgt ttt atg agt cat cac	1845
Ala Lys Val Asn Tyr Val Lys Asn Asn Ile Cys Phe Met Ser His His	
565 570 575 580	
caa gaa gaa tta gtg cca aaa cag cct caa aaa aga aaa ccc cag gag	1893
Gln Glu Glu Leu Val Pro Lys Gln Pro Gln Lys Arg Lys Pro Gln Glu	
585 590 595	
cag ctc ttg gag tgt aac aag ctg tgt ggt agg ggc caa tcc agg cag	1941
Gln Leu Leu Glu Cys Asn Lys Leu Cys Gly Arg Gly Gln Ser Arg Gln	
600 605 610	
ctt tct cca gag acc taa tggcctcaac accttctgaa cgtggatagt	1989
Leu Ser Pro Glu Thr	
615	

gccagaacac ttaggaggggt gtctttggac caatgcatag ttgcgactcc tgtgctctct 2049
 ttccagtgtc atggaactgg ttttgaagag acactctgaa atgataaaga cagcctttaa 2109
 tccccctcct cccagaagg aacctcaaaa ggtagatgag gtacaagggtc ctaagtgatc 2169
 tctttttctg agcaggatat caggcaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 2223

<210> 56
 <211> 617
 <212> PRT
 <213> GLUT12

<400> 56

Met Val Pro Val Glu Asn Thr Glu Gly Pro Ser Leu Leu Asn Gln Lys
 1 5 10 15

Gly Thr Ala Val Glu Thr Glu Gly Ser Gly Ser Arg His Pro Pro Trp
 20 25 30

Ala Arg Gly Cys Gly Met Phe Thr Phe Leu Ser Ser Val Thr Ala Ala
 35 40 45

Val Ser Gly Leu Leu Val Gly Tyr Glu Leu Gly Ile Ile Ser Gly Ala
 50 55 60

Leu Leu Gln Ile Lys Thr Leu Leu Ala Leu Ser Cys His Glu Gln Glu
 65 70 75 80

Met Val Val Ser Ser Leu Val Ile Gly Ala Leu Leu Ala Ser Leu Thr
 85 90 95

Gly Gly Val Leu Ile Asp Arg Tyr Gly Arg Arg Thr Ala Ile Ile Leu
 100 105 110

Ser Ser Cys Leu Leu Gly Leu Gly Ser Leu Val Leu Ile Leu Ser Leu
 115 120 125

Ser Tyr Thr Val Leu Ile Val Gly Arg Ile Ala Ile Gly Val Ser Ile
 130 135 140

Ser Leu Ser Ser Ile Ala Thr Cys Val Tyr Ile Ala Glu Ile Ala Pro
 145 150 155 160

Gln His Arg Arg Gly Leu Leu Val Ser Leu Asn Glu Leu Met Ile Val
 165 170 175

Ile Gly Ile Leu Ser Ala Tyr Ile Ser Asn Tyr Ala Phe Ala Asn Val
 180 185 190

Phe His Gly Trp Lys Tyr Met Phe Gly Leu Val Ile Pro Leu Gly Val
 195 200 205
 Leu Gln Ala Ile Ala Met Tyr Phe Leu Pro Pro Ser Pro Arg Phe Leu
 210 215 220
 Val Met Lys Gly Gln Glu Gly Ala Ala Ser Lys Val Leu Gly Arg Leu
 225 230 235 240
 Arg Ala Leu Ser Asp Thr Thr Glu Glu Leu Thr Val Ile Lys Ser Ser
 245 250 255
 Leu Lys Asp Glu Tyr Gln Tyr Ser Phe Trp Asp Leu Phe Arg Ser Lys
 260 265 270
 Asp Asn Met Arg Thr Arg Ile Met Ile Gly Leu Thr Leu Val Phe Phe
 275 280 285
 Val Gln Ile Thr Gly Gln Pro Asn Ile Leu Phe Tyr Ala Ser Thr Val
 290 295 300
 Leu Lys Ser Val Gly Phe Gln Ser Asn Glu Ala Ala Ser Leu Ala Ser
 305 310 315 320
 Thr Gly Val Gly Val Val Lys Val Ile Ser Thr Ile Pro Ala Thr Leu
 325 330 335
 Leu Val Asp His Val Gly Ser Lys Thr Phe Leu Cys Ile Gly Ser Ser
 340 345 350
 Val Met Ala Ala Ser Leu Val Thr Met Gly Ile Val Asn Leu Asn Ile
 355 360 365
 His Met Asn Phe Thr His Ile Cys Arg Ser His Asn Ser Ile Asn Gln
 370 375 380
 Ser Leu Asp Glu Ser Val Ile Tyr Gly Pro Gly Asn Leu Ser Thr Asn
 385 390 395 400
 Asn Asn Thr Leu Arg Asp His Phe Lys Gly Ile Ser Ser His Ser Arg
 405 410 415
 Ser Ser Leu Met Pro Leu Arg Asn Asp Val Asp Lys Arg Gly Glu Thr
 420 425 430
 Thr Ser Ala Ser Leu Leu Asn Ala Gly Leu Ser His Thr Glu Tyr Gln

115

cgg cgc agg aag cag ccg gag ctg gac gcg gcg agc gcg gcc ggg gag Arg Arg Arg Lys Gln Pro Glu Pro Asp Ala Ala Ser Ala Ala Gly Glu 5 10 15	165
tgc agc ctc ctg gct gcc gcc gaa tcg agc acc agc ctg cag agc gcg Cys Ser Leu Leu Ala Ala Ala Glu Ser Ser Thr Ser Leu Gln Ser Ala 20 25 30 35	213
ggc gcg ggc ggc ggc ggc gtc ggg gac ctg gag cgc gcg gcg cgg cgg Gly Ala Gly Gly Gly Gly Val Gly Asp Leu Glu Arg Ala Ala Arg Arg 40 45 50	261
cag ttc cag cag gac gag acc ccc gcc ttc gtg tac gtg gtg gcc gtc Gln Phe Gln Gln Asp Glu Thr Pro Ala Phe Val Tyr Val Val Ala Val 55 60 65	309
ttc tcc gcg ctg ggc ggc ttc ctg ttt ggc tat gac acc ggg gtg gtg Phe Ser Ala Leu Gly Gly Phe Leu Phe Gly Tyr Asp Thr Gly Val Val 70 75 80	357
tca ggg gcc atg ctg ctg ctc aag cgg cag ctc agt ctg gac gcg ctg Ser Gly Ala Met Leu Leu Leu Lys Arg Gln Leu Ser Leu Asp Ala Leu 85 90 95	405
tgg cag gag ctg ctg gtg tcc agc acg gtg ggg gcg gct gcc gtc tcg Trp Gln Glu Leu Leu Val Ser Ser Thr Val Gly Ala Ala Ala Val Ser 100 105 110 115	453
gcg ctg gcc gga ggc gcc ctc aac ggc gtc ttc ggc cgc cgc gct gcc Ala Leu Ala Gly Gly Ala Leu Asn Gly Val Phe Gly Arg Arg Ala Ala 120 125 130	501
atc ctc ctg gcc agt gcc ctc ttc acc gcc ggc tcc gcg gtg ctg gct Ile Leu Leu Ala Ser Ala Leu Phe Thr Ala Gly Ser Ala Val Leu Ala 135 140 145	549
gcg gcc aac aac aag gag aca ctg ctc gcc ggc cgc ctg gtc gtg gga Ala Ala Asn Asn Lys Glu Thr Leu Leu Ala Gly Arg Leu Val Val Gly 150 155 160	597
ctc ggc atc ggc att gct tct atg aca gtg cca gtg tac att gcg gag Leu Gly Ile Gly Ile Ala Ser Met Thr Val Pro Val Tyr Ile Ala Glu 165 170 175	645
gtc tca cca ccc aat tta aga ggc cga tta gtc acc att aat acc ctc Val Ser Pro Pro Asn Leu Arg Gly Arg Leu Val Thr Ile Asn Thr Leu 180 185 190 195	693
ttc atc aca gga ggg cag ttc ttt gca agt gtt gtt gat gga gcc ttc Phe Ile Thr Gly Gly Gln Phe Phe Ala Ser Val Val Asp Gly Ala Phe 200 205 210	741
agt tat ctc cag aag gat gga tgg agg tac atg ttg gga ctt gca rca Ser Tyr Leu Gln Lys Asp Gly Trp Arg Tyr Met Leu Gly Leu Ala Xaa 215 220 225	789
gtt ccg gcg gtt ata cag ttt ttt ggc ttt ctc ttt ttg cct gaa agc Val Pro Ala Val Ile Gln Phe Phe Gly Phe Leu Phe Leu Pro Glu Ser 230 235 240	837
cct cga tgg ctt att cag aaa gga cag act cag aag gcc cgt aga att Pro Arg Trp Leu Ile Gln Lys Gly Gln Thr Gln Lys Ala Arg Arg Ile	885

116

245	250	255	
tta tct cag atg cgt ggt aac cag acc att gat gag gaa tat gat agc Leu Ser Gln Met Arg Gly Asn Gln Thr Ile Asp Glu Glu Tyr Asp Ser 260 265 270 275			933
atc aaa aac aac att gaa gag gag gaa aaa gag gtt ggc tca gct gga Ile Lys Asn Asn Ile Glu Glu Glu Glu Lys Glu Val Gly Ser Ala Gly 280 285 290			981
cct gtg atc tgc aga atg ctg agt tat ccc cca act cgc cga gct tta Pro Val Ile Cys Arg Met Leu Ser Tyr Pro Pro Thr Arg Arg Ala Leu 295 300 305			1029
att gtg ggt tgt ggc cta caa atg ttc cag cag ctc tca ggc att aac Ile Val Gly Cys Gly Leu Gln Met Phe Gln Gln Leu Ser Gly Ile Asn 310 315 320			1077
acc atc atg tac tac agt gca acc att ctg cag atg tct ggt gtt gaa Thr Ile Met Tyr Tyr Ser Ala Thr Ile Leu Gln Met Ser Gly Val Glu 325 330 335			1125
gat gat aga ctt gca ata tgg ctg gct tca gtt aca gcc ttc aca aat Asp Asp Arg Leu Ala Ile Trp Leu Ala Ser Val Thr Ala Phe Thr Asn 340 345 350 355			1173
ttc att ttc aca ctt gtg gga gtc tgg ctt gtt gag aag gtg ggc cgc Phe Ile Phe Thr Leu Val Gly Val Trp Leu Val Glu Lys Val Gly Arg 360 365 370			1221
aga aag ctt acc ttt ggt agt tta gca ggt acc acc gta gca ctc att Arg Lys Leu Thr Phe Gly Ser Leu Ala Gly Thr Thr Val Ala Leu Ile 375 380 385			1269
att ctt gcc ttg gga ttt gtg cta tca gcc caa gtt tcc cca cgc atc Ile Leu Ala Leu Gly Phe Val Leu Ser Ala Gln Val Ser Pro Arg Ile 390 395 400			1317
act ttt aag cca ata gct ccg tca ggt cag aac gcc act tgc aca aga Thr Phe Lys Pro Ile Ala Pro Ser Gly Gln Asn Ala Thr Cys Thr Arg 405 410 415			1365
tac agt tac tgt aat gaa tgt atg ttg gat cca gac tgc ggt ttc tgc Tyr Ser Tyr Cys Asn Glu Cys Met Leu Asp Pro Asp Cys Gly Phe Cys 420 425 430 435			1413
twc aag atg aac aaa tca act gtc att gac tcc tcc tgt gtt cca gtt Xaa Lys Met Asn Lys Ser Thr Val Ile Asp Ser Ser Cys Val Pro Val 440 445 450			1461
aat aaa gca tct aca aat gag gca gcc tgg ggc agg tgt gaa aat gaa Asn Lys Ala Ser Thr Asn Glu Ala Ala Trp Gly Arg Cys Glu Asn Glu 455 460 465			1509
acc aag ttc aaa aca gaa gat ata ttt tgg gct tac aat ttc tgc cct Thr Lys Phe Lys Thr Glu Asp Ile Phe Trp Ala Tyr Asn Phe Cys Pro 470 475 480			1557
act cca tac tcc tgg act gca ctt ctg ggc ctt att tta tat ctt gtc Thr Pro Tyr Ser Trp Thr Ala Leu Leu Gly Leu Ile Leu Tyr Leu Val 485 490 495			1605
ttc ttt gca cct gga atg gga cca atg cct tgg act gtg aat tct gaa			1653


```

gcccaaatca ctacaccttc ctcatgggcc ttggagtcct actatattgt gccttcattt 2938
gtgttacata catagctgca agcaaaccat ttttcccctt tcttttatc aaacaataat 2998
ttttgaaaca aaaaagagga aggaaatcag tggcagaaat aatcctgctg ttattggtgt 3058
ttgtttaata aaaataatgg gacttttttc ttaacttttt attagctctt cctaagggaa 3118
atgtcacata ttattattta attgtacttg tcttttttta ctttaagagc ataaactcgt 3178
ttttattttg cacacttttc tcattttcct gagaatttac cagaaaaaaaa aagatacata 3238
gatttgtctc tgtgtttttc.tta 3261

```

```

<210> 58
<211> 629
<212> PRT
<213> GLUT13 (HMIT)

```

```

<220>
<221> misc_feature
<222> (227)..(227)
<223> The 'Xaa' at location 227 stands for Ala, or Thr.

```

```

<220>
<221> misc_feature
<222> (436)..(436)
<223> The 'Xaa' at location 436 stands for Tyr, or Phe.

```

```

<400> 58

```

```

Met Gly Glu Arg Arg Arg Lys Gln Pro Glu Pro Asp Ala Ala Ser Ala
1          5          10          15

```

```

Ala Gly Glu Cys Ser Leu Leu Ala Ala Ala Glu Ser Ser Thr Ser Leu
20          25          30

```

```

Gln Ser Ala Gly Ala Gly Gly Gly Val Gly Asp Leu Glu Arg Ala
35          40          45

```

```

Ala Arg Arg Gln Phe Gln Gln Asp Glu Thr Pro Ala Phe Val Tyr Val
50          55          60

```

```

Val Ala Val Phe Ser Ala Leu Gly Gly Phe Leu Phe Gly Tyr Asp Thr
65          70          75          80

```

```

Gly Val Val Ser Gly Ala Met Leu Leu Leu Lys Arg Gln Leu Ser Leu
85          90          95

```

```

Asp Ala Leu Trp Gln Glu Leu Leu Val Ser Ser Thr Val Gly Ala Ala
100         105         110

```

```

Ala Val Ser Ala Leu Ala Gly Gly Ala Leu Asn Gly Val Phe Gly Arg
115         120         125

```

Arg Ala Ala Ile Leu Leu Ala Ser Ala Leu Phe Thr Ala Gly Ser Ala
 130 135 140
 Val Leu Ala Ala Ala Asn Asn Lys Glu Thr Leu Leu Ala Gly Arg Leu
 145 150 155 160
 Val Val Gly Leu Gly Ile Gly Ile Ala Ser Met Thr Val Pro Val Tyr
 165 170 175
 Ile Ala Glu Val Ser Pro Pro Asn Leu Arg Gly Arg Leu Val Thr Ile
 180 185 190
 Asn Thr Leu Phe Ile Thr Gly Gly Gln Phe Phe Ala Ser Val Val Asp
 195 200 205
 Gly Ala Phe Ser Tyr Leu Gln Lys Asp Gly Trp Arg Tyr Met Leu Gly
 210 215 220
 Leu Ala Xaa Val Pro Ala Val Ile Gln Phe Phe Gly Phe Leu Phe Leu
 225 230 235 240
 Pro Glu Ser Pro Arg Trp Leu Ile Gln Lys Gly Gln Thr Gln Lys Ala
 245 250 255
 Arg Arg Ile Leu Ser Gln Met Arg Gly Asn Gln Thr Ile Asp Glu Glu
 260 265 270
 Tyr Asp Ser Ile Lys Asn Asn Ile Glu Glu Glu Glu Lys Glu Val Gly
 275 280 285
 Ser Ala Gly Pro Val Ile Cys Arg Met Leu Ser Tyr Pro Pro Thr Arg
 290 295 300
 Arg Ala Leu Ile Val Gly Cys Gly Leu Gln Met Phe Gln Gln Leu Ser
 305 310 315 320
 Gly Ile Asn Thr Ile Met Tyr Tyr Ser Ala Thr Ile Leu Gln Met Ser
 325 330 335
 Gly Val Glu Asp Asp Arg Leu Ala Ile Trp Leu Ala Ser Val Thr Ala
 340 345 350
 Phe Thr Asn Phe Ile Phe Thr Leu Val Gly Val Trp Leu Val Glu Lys
 355 360 365
 Val Gly Arg Arg Lys Leu Thr Phe Gly Ser Leu Ala Gly Thr Thr Val
 370 375 380

120

Ala Leu Ile Ile Leu Ala Leu Gly Phe Val Leu Ser Ala Gln Val Ser
385 390 395 400

Pro Arg Ile Thr Phe Lys Pro Ile Ala Pro Ser Gly Gln Asn Ala Thr
405 410 415

Cys Thr Arg Tyr Ser Tyr Cys Asn Glu Cys Met Leu Asp Pro Asp Cys
420 425 430

Gly Phe Cys Xaa Lys Met Asn Lys Ser Thr Val Ile Asp Ser Ser Cys
435 440 445

Val Pro Val Asn Lys Ala Ser Thr Asn Glu Ala Ala Trp Gly Arg Cys
450 455 460

Glu Asn Glu Thr Lys Phe Lys Thr Glu Asp Ile Phe Trp Ala Tyr Asn
465 470 475 480

Phe Cys Pro Thr Pro Tyr Ser Trp Thr Ala Leu Leu Gly Leu Ile Leu
485 490 495

Tyr Leu Val Phe Phe Ala Pro Gly Met Gly Pro Met Pro Trp Thr Val
500 505 510

Asn Ser Glu Ile Tyr Pro Leu Trp Ala Arg Ser Thr Gly Asn Ala Cys
515 520 525

Ser Ser Gly Ile Asn Trp Ile Phe Asn Val Leu Val Ser Leu Thr Phe
530 535 540

Leu His Thr Ala Glu Tyr Leu Thr Tyr Tyr Gly Ala Phe Phe Leu Tyr
545 550 555 560

Ala Gly Phe Ala Ala Val Gly Leu Leu Phe Ile Tyr Gly Cys Leu Pro
565 570 575

Glu Thr Lys Gly Lys Lys Leu Glu Glu Ile Glu Ser Leu Phe Asp Asn
580 585 590

Arg Leu Cys Thr Cys Gly Thr Ser Asp Ser Asp Glu Gly Arg Tyr Ile
595 600 605

Glu Tyr Ile Arg Val Lys Gly Ser Asn Tyr His Leu Ser Asp Asn Asp
610 615 620

Ala Ser Asp Val Glu

121

625

<210> 59
 <211> 2118
 <212> DNA
 <213> GLUT14

<220>
 <221> CDS
 <222> (110)..(1603)
 <223>

<400> 59
 agcggggctg agcgaagccg cggggcccaa ccgcagtcgc ggggtctggg aggaagcagt 60
 accttgaaga gaaattggag agggagtcaa ttcctaggat agcagagag atg gac aac 118
 Met Asp Asn
 1
 aga cag aat gtc acc cca gct ctg atc ttt gcc atc aca gtt gct aca 166
 Arg Gln Asn Val Thr Pro Ala Leu Ile Phe Ala Ile Thr Val Ala Thr
 5 10 15
 atc ggc tct ttc cag ttt ggc tac aac act ggg gtc atc aat gct cct 214
 Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile Asn Ala Pro
 20 25 30 35
 gag acg atc ata aag gaa ttt atc aat aaa act ttg acg gac aag gca 262
 Glu Thr Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr Asp Lys Ala
 40 45 50
 aat gcc cct ccc tct gag gtg ctg ctc acg aat ctc tgg tcc ttg tct 310
 Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Asn Leu Trp Ser Leu Ser
 55 60 65
 gtg gcc ata ttt tcc gtc ggg ggt atg atc ggc tcc ttt tcc gtc gga 358
 Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe Ser Val Gly
 70 75 80
 ctc ttt gtt aac cgc ttt ggc agg cgc aat tca atg ctg att gtc aac 406
 Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu Ile Val Asn
 85 90 95
 ctg ttg gct gcc act ggt ggc tgc ctt atg gga ctg tgt aaa ata gct 454
 Leu Leu Ala Ala Thr Gly Gly Cys Leu Met Gly Leu Cys Lys Ile Ala
 100 105 110 115
 gag tca gtt gaa atg ctg atc ctg ggc cgc ttg gtt att ggc ctc ttc 502
 Glu Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile Gly Leu Phe
 120 125 130
 tgc gga ctc tgc aca ggt ttt gtg ccc atg tac att gga gag atc tcg 550
 Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly Glu Ile Ser
 135 140 145
 cct act gcc ctg agg ggt gcc ttt ggc act ctc aac cag ctg ggc ata 598
 Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln Leu Gly Ile
 150 155 160
 gtt att gga att ctg gtg gcc cag atc ttt ggt ctg gaa ctc atc ctt 646
 Val Ile Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu Leu Ile Leu
 165 170 175

122

ggg tct gaa gag cta tgg ccg gtg cta tta ggc ttt acc atc ctt cca Gly Ser Glu Glu Leu Trp Pro Val Leu Leu Gly Phe Thr Ile Leu Pro 180 185 190 195	694
gct atc ctg caa agt gca gcc ctt cca tgt tgc cct gaa agt ccc aga Ala Ile Leu Gln Ser Ala Ala Leu Pro Cys Cys Pro Glu Ser Pro Arg 200 205 210	742
ttt ttg ctc att aac aga aaa aaa gag gag aat gct acg cgg atc ctc Phe Leu Leu Ile Asn Arg Lys Lys Glu Glu Asn Ala Thr Arg Ile Leu 215 220 225	790
cag cgg ttg tgg ggc acc cag gat gta tcc caa gac atc cag gag atg Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile Gln Glu Met 230 235 240	838
aaa gat gag agt gca agg atg tca caa gaa aag caa gtc acc gtg ctg Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val Thr Val Leu 245 250 255	886
gag ctc ttt aga gtg tcc agc tac cga cag ccc atc atc att tcc att Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile Ile Ser Ile 260 265 270 275	934
gtg ctc cag ctc tct cag cag ctc tct ggg atc aat gct gtg ttc tat Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala Val Phe Tyr 280 285 290	982
tac tca aca gga atc ttc aag gat gca ggt gtt caa cag ccc atc tat Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Gln Pro Ile Tyr 295 300 305	1030
gcc acc atc agc gcg ggt gtg gtt aat act atc ttc act tta ctt tct Ala Thr Ile Ser Ala Gly Val Val Asn Thr Ile Phe Thr Leu Leu Ser 310 315 320	1078
cta ttt ctg gtg gaa agg gca gga aga agg act ctg cat atg ata ggc Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His Met Ile Gly 325 330 335	1126
ctt gga ggg atg gct ttt tgt tcc acg ctc atg act gtt tct ttg tta Leu Gly Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val Ser Leu Leu 340 345 350 355	1174
tta aag aat cac tat aat ggg atg agc ttt gtc tgt att ggg gct atc Leu Lys Asn His Tyr Asn Gly Met Ser Phe Val Cys Ile Gly Ala Ile 360 365 370	1222
ttg gtc ttt gtg gcc tgt ttt gaa att gga cca ggc ccc att ccc tgg Leu Val Phe Val Ala Cys Phe Glu Ile Gly Pro Gly Pro Ile Pro Trp 375 380 385	1270
ttt att gtg gcc gaa ctc ttc agc cag ggc ccc cgc cca gct gcg atg Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro Ala Ala Met 390 395 400	1318
gca gtg gcc ggc tgc tcc aac tgg acc tcc aac ttc cta gtc gga ttg Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu Val Gly Leu 405 410 415	1366
ctc ttc ccc tct gct gct tac tat tta gga gcc tac gtt ttt att atc Leu Phe Pro Ser Ala Ala Tyr Tyr Leu Gly Ala Tyr Val Phe Ile Ile	1414

123

420 425 430 435

ttc acc ggc ttc ctc att acc ttc ttg gcc ttt acc ttc ttc aaa gtc 1462
Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe Phe Lys Val
 440 445 450

cct gag acc cgt ggc agg act ttt gag gat atc aca cgg gcc ttt gaa 1510
Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg Ala Phe Glu
 455 460 465

ggg cag gca cac ggt gca gat aga tct ggg aag gac ggc gtc atg ggg 1558
Gly Gln Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly Val Met Gly
 470 475 480

atg aac agc atc gag cct gct aag gag acc acc acc aat gtc taa 1603
Met Asn Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn Val
 485 490 495

gtcatgcctc cttccacctc cctcccggca tgggaaagcc acctctccct caacaaggga 1663

gagactttat caggatgaac ccaggactgc ttctgaatgc tgctacttga tttctttctc 1723

atccccagca ctccatgagc accccaaggc tgcagtttgt tggatcttca atggcttttt 1783

aaattttatt tcctggacat cctcttctgc ttaggagaga ccgagtgaac ctaccttcat 1843

ttcaggaggg attggccgct tggcacatga caactttgcc agcttttcct cccttggggtt 1903

ctgatattgc cgactagag gatataggag aggaaaagta aggtgcagtt gccccaacct 1963

cagacttacc aggaagcaga tacatatgag tgtggaagcc ggaggggtgt tatgtaagag 2023

caccttcctc acttccatac agctctacgc ggcaaattaa cttgagtttt atttatctta 2083

tcctctgggtt taattacata aatatttatt tttta 2118

<210> 60
<211> 497
<212> PRT
<213> GLUT14

<400> 60

Met Asp Asn Arg Gln Asn Val Thr Pro Ala Leu Ile Phe Ala Ile Thr
1 5 10 15

Val Ala Thr Ile Gly Ser Phe Gln Phe Gly Tyr Asn Thr Gly Val Ile
 20 25 30

Asn Ala Pro Glu Thr Ile Ile Lys Glu Phe Ile Asn Lys Thr Leu Thr
 35 40 45

Asp Lys Ala Asn Ala Pro Pro Ser Glu Val Leu Leu Thr Asn Leu Trp
50 55 60

Ser Leu Ser Val Ala Ile Phe Ser Val Gly Gly Met Ile Gly Ser Phe
65 70 75 80

124

Ser Val Gly Leu Phe Val Asn Arg Phe Gly Arg Arg Asn Ser Met Leu
 85 90 95

Ile Val Asn Leu Leu Ala Ala Thr Gly Gly Cys Leu Met Gly Leu Cys
 100 105 110

Lys Ile Ala Glu Ser Val Glu Met Leu Ile Leu Gly Arg Leu Val Ile
 115 120 125

Gly Leu Phe Cys Gly Leu Cys Thr Gly Phe Val Pro Met Tyr Ile Gly
 130 135 140

Glu Ile Ser Pro Thr Ala Leu Arg Gly Ala Phe Gly Thr Leu Asn Gln
 145 150 155 160

Leu Gly Ile Val Ile Gly Ile Leu Val Ala Gln Ile Phe Gly Leu Glu
 165 170 175

Leu Ile Leu Gly Ser Glu Glu Leu Trp Pro Val Leu Leu Gly Phe Thr
 180 185 190

Ile Leu Pro Ala Ile Leu Gln Ser Ala Ala Leu Pro Cys Cys Pro Glu
 195 200 205

Ser Pro Arg Phe Leu Leu Ile Asn Arg Lys Lys Glu Glu Asn Ala Thr
 210 215 220

Arg Ile Leu Gln Arg Leu Trp Gly Thr Gln Asp Val Ser Gln Asp Ile
 225 230 235 240

Gln Glu Met Lys Asp Glu Ser Ala Arg Met Ser Gln Glu Lys Gln Val
 245 250 255

Thr Val Leu Glu Leu Phe Arg Val Ser Ser Tyr Arg Gln Pro Ile Ile
 260 265 270

Ile Ser Ile Val Leu Gln Leu Ser Gln Gln Leu Ser Gly Ile Asn Ala
 275 280 285

Val Phe Tyr Tyr Ser Thr Gly Ile Phe Lys Asp Ala Gly Val Gln Gln
 290 295 300

Pro Ile Tyr Ala Thr Ile Ser Ala Gly Val Val Asn Thr Ile Phe Thr
 305 310 315 320

Leu Leu Ser Leu Phe Leu Val Glu Arg Ala Gly Arg Arg Thr Leu His
 325 330 335

125

Met Ile Gly Leu Gly Gly Met Ala Phe Cys Ser Thr Leu Met Thr Val
 340 345 350

Ser Leu Leu Leu Lys Asn His Tyr Asn Gly Met Ser Phe Val Cys Ile
 355 360 365

Gly Ala Ile Leu Val Phe Val Ala Cys Phe Glu Ile Gly Pro Gly Pro
 370 375 380

Ile Pro Trp Phe Ile Val Ala Glu Leu Phe Ser Gln Gly Pro Arg Pro
 385 390 395 400

Ala Ala Met Ala Val Ala Gly Cys Ser Asn Trp Thr Ser Asn Phe Leu
 405 410 415

Val Gly Leu Leu Phe Pro Ser Ala Ala Tyr Tyr Leu Gly Ala Tyr Val
 420 425 430

Phe Ile Ile Phe Thr Gly Phe Leu Ile Thr Phe Leu Ala Phe Thr Phe
 435 440 445

Phe Lys Val Pro Glu Thr Arg Gly Arg Thr Phe Glu Asp Ile Thr Arg
 450 455 460

Ala Phe Glu Gly Gln Ala His Gly Ala Asp Arg Ser Gly Lys Asp Gly
 465 470 475 480

Val Met Gly Met Asn Ser Ile Glu Pro Ala Lys Glu Thr Thr Thr Asn
 485 490 495

Val

<210> 61

<211> 6126

<212> DNA

<213> Cystic Fibrosis Transmembrane Conductor Regulator (CFTR) delta F508
 mutation

<220>

<221> CDS

<222> (133)..(4572)

<223>

<400> 61

aattggaagc aaatgacatc acagcaggtc agagaaaaag ggttgagcgg caggcaccca 60

gagtagtagg tctttggcat taggagcttg agcccagacg gccctagcag ggaccccagc 120

gcccagagaga cc atg cag agg tcg cct ctg gaa aag gcc agc gtt gtc tcc 171

Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser																
				1			5				10					
aaa	ctt	ttt	ttc	agc	tgg	acc	aga	cca	att	ttg	agg	aaa	gga	tac	aga	219
Lys	Leu	Phe	Phe	Ser	Trp	Thr	Arg	Pro	Ile	Leu	Arg	Lys	Gly	Tyr	Arg	
	15				20						25					
cag	cgc	ctg	gaa	ttg	tca	gac	ata	tac	caa	atc	cct	tct	gtt	gat	tct	267
Gln	Arg	Leu	Glu	Leu	Ser	Asp	Ile	Tyr	Gln	Ile	Pro	Ser	Val	Asp	Ser	
30					35					40					45	
gct	gac	aat	cta	tct	gaa	aaa	ttg	gaa	aga	gaa	tgg	gat	aga	gag	ctg	315
Ala	Asp	Asn	Leu	Ser	Glu	Lys	Leu	Glu	Arg	Glu	Trp	Asp	Arg	Glu	Leu	
				50					55					60		
gct	tca	aag	aaa	aat	cct	aaa	ctc	att	aat	gcc	ctt	cgg	cga	tgt	ttt	363
Ala	Ser	Lys	Lys	Asn	Pro	Lys	Leu	Ile	Asn	Ala	Leu	Arg	Arg	Cys	Phe	
			65					70					75			
ttc	tgg	aga	ttt	atg	ttc	tat	gga	atc	ttt	tta	tat	tta	ggg	gaa	gtc	411
Phe	Trp	Arg	Phe	Met	Phe	Tyr	Gly	Ile	Phe	Leu	Tyr	Leu	Gly	Glu	Val	
		80					85					90				
acc	aaa	gca	gta	cag	cct	ctc	tta	ctg	gga	aga	atc	ata	gct	tcc	tat	459
Thr	Lys	Ala	Val	Gln	Pro	Leu	Leu	Leu	Gly	Arg	Ile	Ile	Ala	Ser	Tyr	
	95					100					105					
gac	ccg	gat	aac	aag	gag	gaa	cgc	tct	atc	gcg	att	tat	cta	ggc	ata	507
Asp	Pro	Asp	Asn	Lys	Glu	Glu	Arg	Ser	Ile	Ala	Ile	Tyr	Leu	Gly	Ile	
110					115					120					125	
ggc	tta	tgc	ctt	ctc	ttt	att	gtg	agg	aca	ctg	ctc	cta	cac	cca	gcc	555
Gly	Leu	Cys	Leu	Leu	Phe	Ile	Val	Arg	Thr	Leu	Leu	Leu	His	Pro	Ala	
				130					135					140		
att	ttt	ggc	ctt	cat	cac	att	gga	atg	cag	atg	aga	ata	gct	atg	ttt	603
Ile	Phe	Gly	Leu	His	His	Ile	Gly	Met	Gln	Met	Arg	Ile	Ala	Met	Phe	
			145					150					155			
agt	ttg	att	tat	aag	aag	act	tta	aag	ctg	tca	agc	cgt	gtt	cta	gat	651
Ser	Leu	Ile	Tyr	Lys	Lys	Thr	Leu	Lys	Leu	Ser	Ser	Arg	Val	Leu	Asp	
		160					165					170				
aaa	ata	agt	att	gga	caa	ctt	gtt	agt	ctc	ctt	tcc	aac	aac	ctg	aac	699
Lys	Ile	Ser	Ile	Gly	Gln	Leu	Val	Ser	Leu	Leu	Ser	Asn	Asn	Leu	Asn	
	175					180					185					
aaa	ttt	gat	gaa	gga	ctt	gca	ttg	gca	cat	ttc	gtg	tgg	atc	gct	cct	747
Lys	Phe	Asp	Glu	Gly	Leu	Ala	Leu	Ala	His	Phe	Val	Trp	Ile	Ala	Pro	
190					195					200					205	
ttg	caa	gtg	gca	ctc	ctc	atg	ggg	cta	atc	tgg	gag	ttg	tta	cag	gcg	795
Leu	Gln	Val	Ala	Leu	Leu	Met	Gly	Leu	Ile	Trp	Glu	Leu	Leu	Gln	Ala	
				210					215					220		
tct	gcc	ttc	tgt	gga	ctt	ggt	ttc	ctg	ata	gtc	ctt	gcc	ctt	ttt	cag	843
Ser	Ala	Phe	Cys	Gly	Leu	Gly	Phe	Leu	Ile	Val	Leu	Ala	Leu	Phe	Gln	
			225					230				235				
gct	ggg	cta	ggg	aga	atg	atg	atg	aag	tac	aga	gat	cag	aga	gct	ggg	891
Ala	Gly	Leu	Gly	Arg	Met	Met	Met	Lys	Tyr	Arg	Asp	Gln	Arg	Ala	Gly	
		240					245					250				

aag atc agt gaa aga ctt gtg att acc tca gaa atg att gaa aat atc Lys Ile Ser Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile 255 260 265	939
caa tct gtt aag gca tac tgc tgg gaa gaa gca atg gaa aaa atg att Gln Ser Val Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile 270 275 280 285	987
gaa aac tta aga caa aca gaa ctg aaa ctg act cgg aag gca gcc tat Glu Asn Leu Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr 290 295 300	1035
gtg aga tac ttc aat agc tca gcc ttc ttc ttc tca ggg ttc ttt gtg Val Arg Tyr Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val 305 310 315	1083
gtg ttt tta tct gtg ctt ccc tat gca cta atc aaa gga atc atc ctc Val Phe Leu Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu 320 325 330	1131
cgg aaa ata ttc acc acc atc tca ttc tgc att gtt ctg cgc atg gcg Arg Lys Ile Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala 335 340 345	1179
gtc act cgg caa ttt ccc tgg gct gta caa aca tgg tat gac tct ctt Val Thr Arg Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu 350 355 360 365	1227
gga gca ata aac aaa ata cag gat ttc tta caa aag caa gaa tat aag Gly Ala Ile Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys 370 375 380	1275
aca ttg gaa tat aac tta acg act aca gaa gta gtg atg gag aat gta Thr Leu Glu Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val 385 390 395	1323
aca gcc ttc tgg gag gag gga ttt ggg gaa tta ttt gag aaa gca aaa Thr Ala Phe Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys 400 405 410	1371
caa aac aat aac aat aga aaa act tct aat ggt gat gac agc ctc ttc Gln Asn Asn Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe 415 420 425	1419
ttc agt aat ttc tca ctt ctt ggt act cct gtc ctg aaa gat att aat Phe Ser Asn Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn 430 435 440 445	1467
ttc aag ata gaa aga gga cag ttg ttg gcg gtt gct gga tcc act gga Phe Lys Ile Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly 450 455 460	1515
gca ggc aag act tca ctt cta atg atg att atg gga gaa ctg gag cct Ala Gly Lys Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro 465 470 475	1563
tca gag ggt aaa att aag cac agt gga aga att tca ttc tgt tct cag Ser Glu Gly Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln 480 485 490	1611
ttt tcc tgg att atg cct ggc acc att aaa gaa aat atc atc ggt gtt Phe Ser Trp Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Gly Val 495 500 505	1659

tcc tat gat gaa tat aga tac aga agc gtc atc aaa gca tgc caa cta Ser Tyr Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu 510 515 520 525	1707
gaa gag gac atc tcc aag ttt gca gag aaa gac aat ata gtt ctt gga Glu Glu Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly 530 535 540	1755
gaa ggt gga atc aca ctg agt gga ggt caa cga gca aga att tct tta Glu Gly Gly Ile Thr Leu Ser Gly Gln Arg Ala Arg Ile Ser Leu 545 550 555	1803
gca aga gca gta tac aaa gat gct gat ttg tat tta tta gac tct cct Ala Arg Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro 560 565 570	1851
ttt gga tac cta gat gtt tta aca gaa aaa gaa ata ttt gaa agc tgt Phe Gly Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys 575 580 585	1899
gtc tgt aaa ctg atg gct aac aaa act agg att ttg gtc act tct aaa Val Cys Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys 590 595 600 605	1947
atg gaa cat tta aag aaa gct gac aaa ata tta att ttg aat gaa ggt Met Glu His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu Gly 610 615 620	1995
agc agc tat ttt tat ggg aca ttt tca gaa ctc caa aat cta cag cca Ser Ser Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro 625 630 635	2043
gac ttt agc tca aaa ctc atg gga tgt gat tct ttc gac caa ttt agt Asp Phe Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser 640 645 650	2091
gca gaa aga aga aat tca atc cta act gag acc tta cac cgt ttc tca Ala Glu Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser 655 660 665	2139
tta gaa gga gat gct cct gtc tcc tgg aca gaa aca aaa aaa caa tct Leu Glu Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser 670 675 680 685	2187
ttt aaa cag act gga gag ttt ggg gaa aaa agg aag aat tct att ctc Phe Lys Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu 690 695 700	2235
aat cca atc aac tct ata cga aaa ttt tcc att gtg caa aag act ccc Asn Pro Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro 705 710 715	2283
tta caa atg aat ggc atc gaa gag gat tct gat gag cct tta gag aga Leu Gln Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg 720 725 730	2331
agg ctg tcc tta gta cca gat tct gag cag gga gag gcg ata ctg cct Arg Leu Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro 735 740 745	2379
cgc atc agc gtg atc agc act ggc ccc acg ctt cag gca cga agg agg Arg Ile Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg	2427

750	755	760	765	
cag tct gtc ctg aac ctg atg aca cac tca gtt aac caa ggt cag aac Gln Ser Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn 770 775 780				2475
att cac cga aag aca aca gca tcc aca cga aaa gtg tca ctg gcc cct Ile His Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro 785 790 795				2523
cag gca aac ttg act gaa ctg gat ata tat tca aga agg tta tct caa Gln Ala Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln 800 805 810				2571
gaa act ggc ttg gaa ata agt gaa gaa att aac gaa gaa gac tta aag Glu Thr Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys 815 820 825				2619
gag tgc ctt ttt gat gat atg gag agc ata cca gca gtg act aca tgg Glu Cys Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr Trp 830 835 840 845				2667
aac aca tac ctt cga tat att act gtc cac aag agc tta att ttt gtg Asn Thr Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val 850 855 860				2715
cta att tgg tgc tta gta att ttt ctg gca gag gtg gct gct tct ttg Leu Ile Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu 865 870 875				2763
gtt gtg ctg tgg ctc ctt gga aac act cct ctt caa gac aaa ggg aat Val Val Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn 880 885 890				2811
agt act cat agt aga aat aac agc tat gca gtg att atc acc agc acc Ser Thr His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser Thr 895 900 905				2859
agt tcg tat tat gtg ttt tac att tac gtg gga gta gcc gac act ttg Ser Ser Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr Leu 910 915 920 925				2907
ctt gct atg gga ttc ttc aga ggt cta cca ctg gtg cat act cta atc Leu Ala Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile 930 935 940				2955
aca gtg tcg aaa att tta cac cac aaa atg tta cat tct gtt ctt caa Thr Val Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln 945 950 955				3003
gca cct atg tca acc ctc aac acg ttg aaa gca ggt ggg att ctt aat Ala Pro Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn 960 965 970				3051
aga ttc tcc aaa gat ata gca att ttg gat gac ctt ctg cct ctt acc Arg Phe Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr 975 980 985				3099
ata ttt gac ttc atc cag ttg tta tta att gtg att gga gct ata gca Ile Phe Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala 990 995 1000 1005				3147
gtt gtc gca gtt tta caa ccc tac atc ttt gtt gca aca gtg cca				3192

Val	Val	Ala	Val	Leu	Gln	Pro	Tyr	Ile	Phe	Val	Ala	Thr	Val	Pro	
				1010					1015					1020	
gtg	ata	gtg	gct	ttt	att	atg	ttg	aga	gca	tat	ttc	ctc	caa	acc	3237
Val	Ile	Val	Ala	Phe	Ile	Met	Leu	Arg	Ala	Tyr	Phe	Leu	Gln	Thr	
				1025					1030					1035	
tca	cag	caa	ctc	aaa	caa	ctg	gaa	tct	gaa	ggc	agg	agt	cca	att	3282
Ser	Gln	Gln	Leu	Lys	Gln	Leu	Glu	Ser	Glu	Gly	Arg	Ser	Pro	Ile	
				1040					1045					1050	
ttc	act	cat	ctt	gtt	aca	agc	tta	aaa	gga	cta	tgg	aca	ctt	cgt	3327
Phe	Thr	His	Leu	Val	Thr	Ser	Leu	Lys	Gly	Leu	Trp	Thr	Leu	Arg	
				1055					1060					1065	
gcc	ttc	gga	cgg	cag	cct	tac	ttt	gaa	act	ctg	ttc	cac	aaa	gct	3372
Ala	Phe	Gly	Arg	Gln	Pro	Tyr	Phe	Glu	Thr	Leu	Phe	His	Lys	Ala	
				1070					1075					1080	
ctg	aat	tta	cat	act	gcc	aac	tgg	ttc	ttg	tac	ctg	tca	aca	ctg	3417
Leu	Asn	Leu	His	Thr	Ala	Asn	Trp	Phe	Leu	Tyr	Leu	Ser	Thr	Leu	
				1085					1090					1095	
cgc	tgg	ttc	caa	atg	aga	ata	gaa	atg	att	ttt	gtc	atc	ttc	ttc	3462
Arg	Trp	Phe	Gln	Met	Arg	Ile	Glu	Met	Ile	Phe	Val	Ile	Phe	Phe	
				1100					1105					1110	
att	gct	gtt	acc	ttc	att	tcc	att	tta	aca	aca	gga	gaa	gga	gaa	3507
Ile	Ala	Val	Thr	Phe	Ile	Ser	Ile	Leu	Thr	Thr	Gly	Glu	Gly	Glu	
				1115					1120					1125	
gga	aga	gtt	ggt	att	atc	ctg	act	tta	gcc	atg	aat	atc	atg	agt	3552
Gly	Arg	Val	Gly	Ile	Ile	Leu	Thr	Leu	Ala	Met	Asn	Ile	Met	Ser	
				1130					1135					1140	
aca	ttg	cag	tgg	gct	gta	aac	tcc	agc	ata	gat	gtg	gat	agc	ttg	3597
Thr	Leu	Gln	Trp	Ala	Val	Asn	Ser	Ser	Ile	Asp	Val	Asp	Ser	Leu	
				1145					1150					1155	
atg	cga	tct	gtg	agc	cga	gtc	ttt	aag	ttc	att	gac	atg	cca	aca	3642
Met	Arg	Ser	Val	Ser	Arg	Val	Phe	Lys	Phe	Ile	Asp	Met	Pro	Thr	
				1160					1165					1170	
gaa	ggt	aaa	cct	acc	aag	tca	acc	aaa	cca	tac	aag	aat	ggc	caa	3687
Glu	Gly	Lys	Pro	Thr	Lys	Ser	Thr	Lys	Pro	Tyr	Lys	Asn	Gly	Gln	
				1175					1180					1185	
ctc	tcg	aaa	gtt	atg	att	att	gag	aat	tca	cac	gtg	aag	aaa	gat	3732
Leu	Ser	Lys	Val	Met	Ile	Ile	Glu	Asn	Ser	His	Val	Lys	Lys	Asp	
				1190					1195					1200	
gac	atc	tgg	ccc	tca	ggg	ggc	caa	atg	act	gtc	aaa	gat	ctc	aca	3777
Asp	Ile	Trp	Pro	Ser	Gly	Gly	Gln	Met	Thr	Val	Lys	Asp	Leu	Thr	
				1205					1210					1215	
gca	aaa	tac	aca	gaa	ggt	gga	aat	gcc	ata	tta	gag	aac	att	tcc	3822
Ala	Lys	Tyr	Thr	Glu	Gly	Gly	Asn	Ala	Ile	Leu	Glu	Asn	Ile	Ser	
				1220					1225					1230	
ttc	tca	ata	agt	cct	ggc	cag	agg	gtg	ggc	ctc	ttg	gga	aga	act	3867
Phe	Ser	Ile	Ser	Pro	Gly	Gln	Arg	Val	Gly	Leu	Leu	Gly	Arg	Thr	
				1235					1240					1245	

131

gga tca ggg aag agt act ttg tta tca gct ttt ttg aga cta ctg	3912
Gly Ser Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu	
1250 1255 1260	
aac act gaa gga gaa atc cag atc gat ggt gtg tct tgg gat tca	3957
Asn Thr Glu Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser	
1265 1270 1275	
ata act ttg caa cag tgg agg aaa gcc ttt gga gtg ata cca cag	4002
Ile Thr Leu Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln	
1280 1285 1290	
aaa gta ttt att ttt tct gga aca ttt aga aaa aac ttg gat ccc	4047
Lys Val Phe Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro	
1295 1300 1305	
tat gaa cag tgg agt gat caa gaa ata tgg aaa gtt gca gat gag	4092
Tyr Glu Gln Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp Glu	
1310 1315 1320	
gtt ggg ctc aga tct gtg ata gaa cag ttt cct ggg aag ctt gac	4137
Val Gly Leu Arg Ser Val Ile Glu Gln Phe Pro Gly Lys Leu Asp	
1325 1330 1335	
ttt gtc ctt gtg gat ggg ggc tgt gtc cta agc cat ggc cac aag	4182
Phe Val Leu Val Asp Gly Gly Cys Val Leu Ser His Gly His Lys	
1340 1345 1350	
cag ttg atg tgc ttg gct aga tct gtt ctc agt aag gcg aag atc	4227
Gln Leu Met Cys Leu Ala Arg Ser Val Leu Ser Lys Ala Lys Ile	
1355 1360 1365	
ttg ctg ctt gat gaa ccc agt gct cat ttg gat cca gta aca tac	4272
Leu Leu Leu Asp Glu Pro Ser Ala His Leu Asp Pro Val Thr Tyr	
1370 1375 1380	
caa ata att aga aga act cta aaa caa gca ttt gct gat tgc aca	4317
Gln Ile Ile Arg Arg Thr Leu Lys Gln Ala Phe Ala Asp Cys Thr	
1385 1390 1395	
gta att ctc tgt gaa cac agg ata gaa gca atg ctg gaa tgc caa	4362
Val Ile Leu Cys Glu His Arg Ile Glu Ala Met Leu Glu Cys Gln	
1400 1405 1410	
caa ttt ttg gtc ata gaa gag aac aaa gtg cgg cag tac gat tcc	4407
Gln Phe Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr Asp Ser	
1415 1420 1425	
atc cag aaa ctg ctg aac gag agg agc ctc ttc cgg caa gcc atc	4452
Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala Ile	
1430 1435 1440	
agc ccc tcc gac agg gtg aag ctc ttt ccc cac cgg aac tca agc	4497
Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser	
1445 1450 1455	
aag tgc aag tct aag ccc cag att gct gct ctg aaa gag gag aca	4542
Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr	
1460 1465 1470	
gaa gaa gag gtg caa gat aca agg ctt tag agagcagcat aaatgttgac	4592
Glu Glu Glu Val Gln Asp Thr Arg Leu	
1475	

atgggacatt tgctcatgga attggagctc gtgggacagt cacctcatgg aattggagct 4652
 cgtggaacag ttacctctgc ctcagaaaac aaggatgaat taagtttttt tttaaaaaag 4712
 aaacatttgg taaggggaat .tgaggacact gatatgggtc ttgataaatg gcttcctggc 4772
 aatagtcaaa ttgtgtgaaa ggtacttcaa atccttgaag atttaccact tgtgttttgc 4832
 aagccagatt ttcttgaaaa cccttgccat gtgctagtaa ttggaaaggc agctctaaat 4892
 gtcaatcagc ctagttgatc agcttattgt ctagtgaaac tcgttaattt gtagtgttgg 4952
 agaagaactg aaatcatact tcttaggggtt atgattaagt aatgataact ggaaacttca 5012
 gcggtttata taagcttgta ttcccttttc tctcctctcc ccatgatgtt tagaaacaca 5072
 actatattgt ttgctaagca ttccaactat ctcatctcca agcaagtatt agaataccac 5132
 aggaaccaca agactgcaca tcaaaatatg cccattcaa catctagtga gcagtcagga 5192
 aagagaactt ccagatcctg gaaatcaggg ttagtattgt ccaggcttac caaaaatctc 5252
 aatatttcag ataatcacia tacatccctt acctgggaaa gggctgttat aatctttcac 5312
 aggggacagg atggttcctt tgatgaagaa gttgatatgc cttttccaa ctccagaaag 5372
 tgacaagctc acagaccttt gaactagagt ttagctggaa aagtatgtta gtgcaaattg 5432
 tcacaggaca gcccttcttt ccacagaagc tccaggtaga ggggtgtgta gtagataggc 5492
 catgggcact gtgggtagac acacatgaag tccaagcatt tagatgtata ggttgatggg 5552
 ggtatgtttt caggctagat gtatgtactt catgctgtct aactaagag agaatgagag 5612
 acacactgaa gaagcaccaa tcatgaatta gttttatatg cttctgtttt ataattttgt 5672
 gaagcaaaat tttttctcta ggaaatattt attttaataa tgtttcaaac atatattaca 5732
 atgctgtatt ttaaaagaat gattatgaat tacatttgta taaaataatt tttatatttg 5792
 aaatattgac tttttatggc actagtattt ttatgaaata ttatgttaaa actgggacag 5852
 gggagaacct aggggtgatat taaccagggg ccatgaatca ccttttggtc tggagggaag 5912
 ccttggggct gatcgagttg ttgccacag ctgtatgatt ccagccaga cacagcctct 5972
 tagatgcagt tctgaagaag atggtaccac cagtctgact gtttccatca agggtagact 6032
 gccttctcaa ctccaaactg actcttaaga agactgcatt atatttatta ctgtaagaaa 6092
 atatcacttg tcaataaaat ccatacattt gtgt 6126

<210> 62

<211> 1479

<212> PRT

<213> Cystic Fibrosis Transmembrane Conductor Regulator (CFTR) delta F508 mutation

<400> 62

Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe

133

1	5	10	15
Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg Gln Arg Leu	20	25	30
Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser Ala Asp Asn	35	40	45
Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu Ala Ser Lys	50	55	60
Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg	65	70	75
Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala	85	90	95
Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp	100	105	110
Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys	115	120	125
Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly	130	135	140
Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile	145	150	155
Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser	165	170	175
Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp	180	185	190
Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val	195	200	205
Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe	210	215	220
Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu	225	230	235
Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser	245	250	255

134

Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile Gln Ser Val
 260 265 270

Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu
 275 280 285

Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr
 290 295 300

Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val Val Phe Leu
 305 310 315 320

Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile
 325 330 335

Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg
 340 345 350

Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu Gly Ala Ile
 355 360 365

Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys Thr Leu Glu
 370 375 380

Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val Thr Ala Phe
 385 390 395 400

Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys Gln Asn Asn
 405 410 415

Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe Phe Ser Asn
 420 425 430

Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn Phe Lys Ile
 435 440 445

Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly Ala Gly Lys
 450 455 460

Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro Ser Glu Gly
 465 470 475 480

Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln Phe Ser Trp
 485 490 495

Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Gly Val Ser Tyr Asp
 500 505 510

135

Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu Glu Glu Asp
 515 520 525

Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly Gly
 530 535 540

Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg Ala
 545 550 555 560

Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly Tyr
 565 570 575

Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys Lys
 580 585 590

Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu His
 595 600 605

Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu Gly Ser Ser Tyr
 610 615 620

Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe Ser
 625 630 635 640

Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu Arg
 645 650 655

Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu Gly
 660 665 670

Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys Gln
 675 680 685

Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro Ile
 690 695 700

Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln Met
 705 710 715 720

Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg Arg Leu Ser
 725 730 735

Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro Arg Ile Ser
 740 745 750

Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg Gln Ser Val
 755 760 765

Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn Ile His Arg
 770 775 780

Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro Gln Ala Asn
 785 790 795 800

Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln Glu Thr Gly
 805 810 815

Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys Glu Cys Leu
 820 825 830

Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr Trp Asn Thr Tyr
 835 840 845

Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val Leu Ile Trp
 850 855 860

Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu Val Val Leu
 865 870 875 880

Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn Ser Thr His
 885 890 895

Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser Thr Ser Ser Tyr
 900 905 910

Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr Leu Leu Ala Met
 915 920 925

Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile Thr Val Ser
 930 935 940

Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln Ala Pro Met
 945 950 955 960

Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe Ser
 965 970 975

Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe Asp
 980 985 990

Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val Ala
 995 1000 1005

Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro Val Ile Val

137

1010	1015	1020
Ala Phe Ile Met Leu Arg 1025	Ala Tyr Phe Leu Gln Thr 1030	Ser Gln Gln 1035
Leu Lys Gln Leu Glu Ser 1040	Glu Gly Arg Ser Pro 1045	Ile Phe Thr His 1050
Leu Val Thr Ser Leu Lys 1055	Gly Leu Trp Thr Leu 1060	Arg Ala Phe Gly 1065
Arg Gln Pro Tyr Phe Glu 1070	Thr Leu Phe His Lys 1075	Ala Leu Asn Leu 1080
His Thr Ala Asn Trp Phe 1085	Leu Tyr Leu Ser Thr 1090	Leu Arg Trp Phe 1095
Gln Met Arg Ile Glu Met 1100	Ile Phe Val Ile Phe 1105	Phe Ile Ala Val 1110
Thr Phe Ile Ser Ile Leu 1115	Thr Gly Glu Gly 1120	Glu Gly Arg Val 1125
Gly Ile Ile Leu Thr Leu 1130	Ala Met Asn Ile Met 1135	Ser Thr Leu Gln 1140
Trp Ala Val Asn Ser Ser 1145	Ile Asp Val Asp Ser 1150	Leu Met Arg Ser 1155
Val Ser Arg Val Phe Lys 1160	Phe Ile Asp Met Pro 1165	Thr Glu Gly Lys 1170
Pro Thr Lys Ser Thr Lys 1175	Pro Tyr Lys Asn Gly 1180	Gln Leu Ser Lys 1185
Val Met Ile Ile Glu Asn 1190	Ser His Val Lys Lys 1195	Asp Asp Ile Trp 1200
Pro Ser Gly Gly Gln Met 1205	Thr Val Lys Asp Leu 1210	Thr Ala Lys Tyr 1215
Thr Glu Gly Gly Asn Ala 1220	Ile Leu Glu Asn Ile 1225	Ser Phe Ser Ile 1230
Ser Pro Gly Gln Arg Val 1235	Gly Leu Leu Gly Arg 1240	Thr Gly Ser Gly 1245

138

Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu Asn Thr Glu
 1250 1255 1260
 Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile Thr Leu
 1265 1270 1275
 Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val Phe
 1280 1285 1290
 Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln
 1295 1300 1305
 Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu
 1310 1315 1320
 Arg Ser Val Ile Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu
 1325 1330 1335
 Val Asp Gly Gly Cys Val Leu Ser His Gly His Lys Gln Leu Met
 1340 1345 1350
 Cys Leu Ala Arg Ser Val Leu Ser Lys Ala Lys Ile Leu Leu Leu
 1355 1360 1365
 Asp Glu Pro Ser Ala His Leu Asp Pro Val Thr Tyr Gln Ile Ile
 1370 1375 1380
 Arg Arg Thr Leu Lys Gln Ala Phe Ala Asp Cys Thr Val Ile Leu
 1385 1390 1395
 Cys Glu His Arg Ile Glu Ala Met Leu Glu Cys Gln Gln Phe Leu
 1400 1405 1410
 Val Ile Glu Glu Asn Lys Val Arg Gln Tyr Asp Ser Ile Gln Lys
 1415 1420 1425
 Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala Ile Ser Pro Ser
 1430 1435 1440
 Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser Lys Cys Lys
 1445 1450 1455
 Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr Glu Glu Glu
 1460 1465 1470
 Val Gln Asp Thr Arg Leu
 1475

<210> 63
<211> 36
<212> DNA
<213> synthetic oligonucleotide

<400> 63
tgagatcgat tacccttatg atgttcctga ttatgg 36

<210> 64
<211> 36
<212> DNA
<213> synthetic oligonucleotide

<400> 64
tcagcataat caggaacatc ataaggataa tcgac 36